

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 13:02:49 ; Search time 104 Seconds
(without alignments)
6548.598 Million cell updates/sec

Title: US-09-891-138A-1
Perfect score: 1543
Sequence: 1 gctcctggcagagttttctg.....tgccataaataaatcaatata 1543

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	589.2	38.2	1996	2	US-08-559-524A-1	Sequence 1, Appli	
2	589.2	38.2	1996	3	US-08-749-707-1	Sequence 1, Appli	
3	88.4	5.7	1429	4	US-09-016-434-1068	Sequence 1068, Ap	
4	86.4	5.6	3055	4	US-09-016-434-1456	Sequence 1456, Ap	
5	85.4	5.5	2025	4	US-09-016-434-1482	Sequence 1482, Ap	
6	82.8	5.4	1571	4	US-09-016-434-1108	Sequence 1108, Ap	
7	82.2	5.3	1805	4	US-08-405-271A-18	Sequence 18, Appl	
8	82.2	5.3	1973	4	US-09-016-434-1391	Sequence 1391, Ap	
9	80	5.2	1586	1	US-08-461-244-1	Sequence 1, Appli	
10	80	5.2	1953	4	US-09-016-434-1096	Sequence 1096, Ap	
11	79.6	5.2	984	3	US-08-513-974B-57	Sequence 57, Appl	

12	79.6	5.2	984	4	US-09-461-436B-57	Sequence 57, Appl
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14	79.2	5.1	998	4	US-08-432-174A-3	Sequence 3, Appli
15	78.4	5.1	1495	4	US-09-016-434-1190	Sequence 1190, Ap
16	78.4	5.1	2156	1	US-08-012-988A-1	Sequence 1, Appli
17	78	5.1	1640	3	US-08-781-250-1	Sequence 1, Appli
18	77.6	5.0	1773	4	US-09-016-434-1405	Sequence 1405, Ap
19	76	4.9	1679	4	US-09-016-434-1097	Sequence 1097, Ap
20	76	4.9	2100	4	US-09-495-050A-289	Sequence 289, App
21	74.8	4.8	984	3	US-08-459-046-1	Sequence 1, Appli
22	74.8	4.8	984	4	US-09-102-710B-1	Sequence 1, Appli
23	74.2	4.8	1140	4	US-09-016-434-750	Sequence 750, App
24	74.2	4.8	1301	2	US-08-467-948A-7	Sequence 7, Appli
25	74.2	4.8	1301	3	US-08-467-947A-7	Sequence 7, Appli
26	74	4.8	1086	4	US-09-170-496D-77	Sequence 77, Appl
27	74	4.8	1086	4	US-09-170-496D-205	Sequence 205, App
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33	73.8	4.8	1065	3	US-08-847-296B-2	Sequence 2, Appli
34	73.8	4.8	1071	4	US-08-567-882-6	Sequence 6, Appli
35	73.8	4.8	1116	4	US-08-720-565-5	Sequence 5, Appli
36	73.8	4.8	1193	4	US-08-720-565-3	Sequence 3, Appli
37	73.8	4.8	1201	4	US-09-016-434-1085	Sequence 1085, Ap
38	73.8	4.8	1689	4	US-08-720-565-1	Sequence 1, Appli
39	73.8	4.8	1915	3	US-08-575-967A-3	Sequence 3, Appli
40	72	4.7	1147	1	US-08-417-103-15	Sequence 15, Appl
41	72	4.7	1351	1	US-07-816-283-5	Sequence 5, Appli
42	72	4.7	1351	1	US-08-417-103-5	Sequence 5, Appli
43	72	4.7	1351	4	US-09-016-434-1303	Sequence 1303, Ap
44	71.4	4.6	1796	1	US-07-816-283-11	Sequence 11, Appl
45	71.4	4.6	1796	1	US-08-417-103-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-559-524A-1

; Sequence 1, Application US/08559524A

; Patent No. 5871963

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.

; APPLICANT: Jantzen, Hans-Michael

; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1996 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  625..1626
US-08-559-524A-1

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Query Match          38.2%;  Score 589.2;  DB 2;  Length 1996;
Best Local Similarity 75.1%;  Pred. No. 5.3e-156;
Matches 762;  Conservative 0;  Mismatches 248;  Indels 4;  Gaps 2;

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Db      632 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 691

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158
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Db      692 AGTACTACCTTTCCATTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGAAATACCA 751

Qy      159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
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Qy      219 TTAACCTTTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
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; ZIP: 20036-5869
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 625..1626
US-08-749-707-1

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Query Match          38.2%; Score 589.2; DB 3; Length 1996;
Best Local Similarity 75.1%; Pred. No. 5.3e-156;
Matches 762; Conservative 0; Mismatches 248; Indels 4; Gaps 2;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
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Db      632 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 691

Qy      99 AGTACTACCTCTCTGCATTTTTATGCAATCGAGTTCATTTTTTGGACTGCTTGGGAATGTCA 158
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Qy     159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
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Db      752 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 811

Qy     219 TTAACCTTTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
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Db      812 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 871

Qy     279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
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Db      872 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 931

Qy     339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGC 398
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Db      932 ATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA 991

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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1068:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1124904
US-09-016-434-1068

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Query Match          5.7%; Score 88.4; DB 4; Length 1429;
Best Local Similarity 45.7%; Pred. No. 5.6e-15;
Matches 385; Conservative 0; Mismatches 451; Indels 6; Gaps 2;

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Qy      167 TTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCTT 226
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Db      352 TGGCTCTTCATCTTCCGCCTCCGACCCTGGGATGCAACGGCCACCTACATGTTCACCTG 411

Qy      227 TCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTAT---GCC 283
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Db      412 GCATTGTGAGACACCTTGTATGTGCTGTGCGCTGCCCCACCCTCATCTACTATATGCAGCC 471

Qy      284 AATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACC 343
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Db      472 CACAACCACTGGCCCTTTGGCACTGAGATCTGCAAGTTCGTCCGCTTTCTTTTCTATTGG 531

Qy      344 AACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATG 403

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Db      532 AACCTCTACTGCAGTGTCTTTTCCTCACCTGCATCAGCGTGCACCGCTACCTGGGCATC 591
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Db      592 TGCCACCCACTTCGGGCACCTACGCTGGGGCCGCCCTCGCCTCGCAGGCCTTCTCTGCCTG 651
Qy      464 GCTGTCTGGGCCTTAGTGACCTTAGAAGTTCACCCATGCTCACTTTCATCAATTCTGTC 523
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Qy      524 CCAAAGAAGAGGGCAGTAAGTGCATCGACTATGCAAGTTCCTGGAACCCCTGAACACAAT 583
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Qy      584 CTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGC 643
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Db      772 GTGCACTTCAGCTCGGCGGTGCATGGGGCTGCTCTTTGGCGTGCCCTGCCTGGTCACTCTT 831
Qy      644 TTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGCCAGCAGCAAGCAACTGCC 703
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Db      832 GTTTGCTATGGACTCATGGCTCGTCGCCTGTATCAGCCCTTGCCAGGCTCTGCACAGTCG 891
Qy      704 CTGCCACTGGACAAACCCCAACGCCCTGGTGGTCTGCGGTTGTGATCTTCTCTATACTC 763
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Db      892 TCTTCTCGCCTCCGCTCTCTCCGCACCATAGCTGTGGTGCTGACTGTCTTTGCTGTCTGC 951
Qy      764 TTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCA 823
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Qy      824 CAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTCTGGCCTTT 883
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Qy      884 CTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAGATG 943
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Qy      944 CT 945
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Db      1129 CT 1130

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RESULT 4

US-09-016-434-1456

; Sequence 1456, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1456:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3055 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g798835
US-09-016-434-1456

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Query Match          5.6%; Score 86.4; DB 4; Length 3055;
Best Local Similarity 46.1%; Pred. No. 3.1e-14;
Matches 402; Conservative 0; Mismatches 461; Indels 9; Gaps 3;

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Qy      140 GGA CTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAAC 199
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Db      1042 GGCTTCCTGGGCAACAGCGTGGCCATCTGGATGTTTCGTCTTCCACATGAAGCCCTGGAGC 1101

Qy      200 AGCAGCAATGTCTATCTTTTTTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTT 259
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Db      1102 GGCATCTCCGTGTACATGTTCAATTTGGCTCTGGCCGACTTCTTGACGTGCTGACTCTG 1161

Qy      260 CCCATCCTGATAAAGAGTTATGCCAATGATA---AGGGGACCTATGGAGATGTTCTCTGT 316
      || ||||| || |||| | | | ||| || || ||| | |||
Db      1162 CCAGCCCTGATCTTCTACTACTTCAATAAAACAGACTGGATCTTCGGGGATGCCATGTGT 1221

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 Db 1399 CCCATCCTCTTCTACTCAGGTACCGGGGTCCGCAAAAACAAAACCATCACCTGTTACGAC 1458
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RESULT 5

US-09-016-434-1482

; Sequence 1482, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

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; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2025 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g984506
US-09-016-434-1482

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Query Match          5.5%; Score 85.4; DB 4; Length 2025;
Best Local Similarity 46.5%; Pred. No. 4.7e-14;
Matches 389; Conservative 0; Mismatches 436; Indels 12; Gaps 3;

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Qy      91 CTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGG 150
        ||| || |   || ||| | || | | || || | ||| ||| |
Db      335 CTTCAAGTACGTGCTGCTGCCTGTGTCTACGGCGTGGTGTGCGTGCTTGGGCTGTGTCT 394

Qy     151 GAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGT 210
        ||| | | | | | | | | | | | | | | | | | | |
Db     395 GAACGCCGTGGCGCTCTACATCTTCTTGTGCCGCCCTCAAGACCTGGAATGCGTCCACCAC 454

Qy     211 CTATCTTTTAACTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGAT 270
        ||| | || |||| | | |||| | | | | ||| || | ||| |
Db     455 ATATATGTTCCACCTGGCTGTGTCTGATGCACTGTATGCGGCCCTCCCTGCCGCTGCTGGT 514

Qy     271 AAAGAGTTATGCCAAT--GATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCG 327
        |   || |||   || | || || | | | |||| | | |
Db     515 CTATTACTACGCCCCGCGCGACCACTGGCCCTTCAGCACGGTGCTCTGCAAGCTGGTGCG 574

Qy     328 ATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATGGA 387
        | | | | |||| |||| ||| |||| |||| |||| | ||| ||| || |
Db     575 CTCCTCTTCTACACCAACCTTTACTGCAGCATCCTCTTCCTCACCTGCATCAGCGTGCA 634

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Qy 388 CCGATATCTGCTCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGC 447
 ||| | ||| | | ||| | | | | | | |
 Db 635 CCGGTGTCTGGGCGTCTTACGACCTCTGCGCTCCCTGCGCTGGGGCCGGGCCCGCTACGC 694
 Qy 448 CATTTTAATCTCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCAC 507
 | | | | | | | | | | | | | | |
 Db 695 TCGCCGGGTGGCCGGGGCCGTGTGGGTGTTGGTGCTGGCCTGCCAGGCCCCCGTGCTCTA 754
 Qy 508 TTTTCATCAATTCTGTCCCAAAGAAGAGGGCAGTAACATGCATCGACTATGCAAGTTCTGG 567
 || ||| | | | | | | | | | | | | | | |
 Db 755 CTTTGTCAACCACAGCGCGCGGGGGCCGCGTAACCTGCCACGACACCTCGGCACCCGA 814
 Qy 568 AAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCC 627
 | | | | | | | | | | | | | | | | | |
 Db 815 GCTCTTCAGCCGCTTCGTGGCCTACAGCTCAGTCATGCTGGGCCTGCTCTTCGCGGTGCC 874
 Qy 628 TCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCA 687
 | | ||| | | ||| | | ||| | | | | | | |
 Db 875 CTTTGCCGTCACTCCTTGTCTGTTACGTGCTCATGGCTCGGCGACTGCTAAAGCCAGCCTA 934
 Qy 688 GCAGCAAGCAACTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGT 747
 | | | | | | | | | | | | | | | | | |
 Db 935 CGGGACCTCGGGCGGCCTCCCTAGGGCCAAGCGCAAGTCCGTGCGCACCATCGCCGTGGT 994
 Qy 748 G-----ATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGC 801
 | | ||| | | ||| | | | | | | | | | |
 Db 995 GCTGGCTGTCTTCGCCCTCTGCTTCCTGCCATTCCACGTACCCGACCCCTCTACTACTC 1054
 Qy 802 CTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACAC 861
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 Db 1055 CTTCCGCTCGCTGG---ACCTCAGCTGCCACACCCTCAACGCCATCAACATGGCCTACAA 1111
 Qy 862 ACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCT 918
 | | ||| | | ||| | | ||| | | | | | | |
 Db 1112 GGTACCCGGCCGCTGGCCAGTGCTAACAGTTGCCTTGACCCCGTGCTCTACTTCCT 1168

RESULT 6

US-09-016-434-1108

; Sequence 1108, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk


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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HERewith
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;      INFORMATION FOR SEQ ID NO:  1108:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1571 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1296659
US-09-016-434-1108

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Query Match          5.4%;  Score 82.8;  DB 4;  Length 1571;
Best Local Similarity 46.2%;  Pred. No. 2.2e-13;
Matches 390;  Conservative 0;  Mismatches 442;  Indels 12;  Gaps 3;

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Qy      89  ATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTT 148
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Db      343  AACTTCAAGCAACTGCTGCTGCCACCTGTGTATTTCGGCGGTGCTGGCGGCTGGCCTGCCG 402

Qy      149  GGAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAAT 208
      ||| || ||| | | | | | | | | | | | | | | |
Db      403  CTGAACATCTGTGTCATTACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCC 462

Qy      209  GTCTATCTTTTAAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTG 268
      || ||      | ||||| | | | |||| | | | | ||| ||| |||
Db      463  GTGTACACCCTAAACCTTGCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCTGCTC 522

Qy      269  ATAAAGAGTTATGCCAA---TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAAC 325
      || | | ||||| | ||| | | ||| ||| | | ||| |
Db      523  ATCTACAACCTATGCCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCTGGTC 582

Qy      326  CGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATG 385
      || | | | | ||||| || ||||| ||||| ||||| ||| ||| |
Db      583  CGCTTCCTCTTCTATGCCAACCTGCACGGCAGCATCCTCTTCCTCACCTGCATCAGCTTC 642

Qy      386  GACCGATATCTGCTCATGAAGTACCCTTT---CCGAGAACACTTTCTACAAAAGAAGGAA 442
      | || || ||| ||| |||| | || ||| |
Db      643  CAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCCGCCGG 702

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Qy	443	TTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATG	502
Db	703	GCTGCCTGGCTAGTGTGTGTAGCCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCCACA	762
Qy	503	CTCACTTTTCATCAATTCTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGT	562
Db	763	GCCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTGTCTATGACCTCAGCCCG	822
Qy	563	TCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTA	622
Db	823	CCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTG	882
Qy	623	ATTCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGG	682
Db	883	CTGCCCTTTGCTGCCCTGCTGGCTGCTACTGTCTCTCTGGCCTGCCGCTGTGCCGCCAG	942
Qy	683	AGCCAGCAGCAAGCAACTG-----CCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC	736
Db	943	GATGGCCCCGGCAGAGCCTGTGGCCAGGAGCGCGTGGCAAGGCGGCCCCGCATGGCCGTG	1002
Qy	737	CTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG	796
Db	1003	GTGGTGGCTGCTGCCTTTGCCATCAGCTTCTGCTTTTCACATCACCAAGACAGCCTAC	1062
Qy	797	ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA	856
Db	1063	CTGGCAGTGCGCTCGACGCCGGGCGTCCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCC	1122
Qy	857	TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC	916
Db	1123	TACAAAGGCACGCGGCCGTTTGCCAGTGCCAACAGCGTGCTGGACCCCATCCTCTTCTAC	1182
Qy	917	CTCA	920
Db	1183	TTCA	1186

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS

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;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/405,271A
;   FILING DATE: 14-MAR-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MURASHIGE, KATE H.
;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 22000-20526.22
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 887-1500
;   TELEFAX: (202) 887-0763
;   TELEX: 90-4030 MRSNFOERSWSH
;   INFORMATION FOR SEQ ID NO: 18:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1805 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 10..1119
US-08-405-271A-18

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Query Match          5.3%; Score 82.2; DB 4; Length 1805;
Best Local Similarity 44.5%; Pred. No. 3.5e-13;
Matches 379; Conservative 0; Mismatches 463; Indels 9; Gaps 1;

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Qy      85 GGCTATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACT 144
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Db      147 GCCCCTCGGGCTCAAGGTCACCATCGTGGGGCTCTACCTGGCCGTGTGTGTCGGAGGGCT 206

Qy      145 GCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAG 204
      | | | | | | | | | | | | | | | | | | | | | |
Db      207 CCTGGGGAACCTGCCTTGTATGTACGTCATCCTCAGGCACACCAAATGAAGACAGCCAC 266

Qy      205 CAATGTCTATCTTTTAAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCCTTCCCAT 264
      | | | | | | | | | | | | | | | | | | | | | |
Db      267 CAATATTTACATCTTTAAACCTGGCCCTGGCCGACACTCTGGTCTGCTGACGCTGCCCTT 326

Qy      265 CCTGATAAAGAGTTATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAA 324
      | | | | | | | | | | | | | | | | | | | | | |
Db      327 CCAGGGCACGGACATCCTCCTGGGCTTCTGGCCGTTTGGGAATGCGCTGTGCAAGACAGT 386

Qy      325 CCGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCAT 384
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Db      387 CATTGCCATTGACTACTACAACATGTTACACGACCTTCACCCTAAGTCCCATGAGTGT 446

Qy      385 GGACCGATATCTGCTCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATT 444
      | | | | | | | | | | | | | | | | | | | | | |
Db      447 GGATCGCTATGTAGCCATCTGCCACCCATCCGTGCCCTCGACGTCCGCACGTCCAGCAA 506

Qy      445 TGCCATTTTAAATCTCGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATGCT 504
      | | | | | | | | | | | | | | | | | | | | | |
Db      507 AGCCCAGGCTGTCAATGTGGCCATCTGGGCCCTGGCCTCTGTTGTGCGGTGTTCCCGTTGC 566

Qy      505 CACTTTCATCAATTCTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTC 564

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Db 567 CATCATGGGCTCGGCACAGGTCGAGGATGAAGAGATCGAGTGCCTGGTGGAGATCCCTAC 626
 Qy 565 TGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAAT 624
 Db 627 CCCTCAGGATTACTGGGGCCCCGGTGTTCGCCATCTGCATCTTCCTCTTCTCCTTCATCGT 686
 Qy 625 TCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAG 684
 Db 687 CCCCCTGCTCGTCATCTCTGTCTGCTACAGCCTCATGATCCGGCGGCTCCGTGGAGTCCG 746
 Qy 685 CCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGT 744
 Db 747 CCTGCTCTCGGGCTCCCAGAGAAGGACCGGAACCTGCGGCGCATCACTCGGCTGGTGCT 806
 Qy 745 TGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTC 804
 Db 807 GGTGGTAGTGGCTGTGTTTCGTGGGCTGCTGGACGCCTGTCCAGGTCTTCGTGCTGGCCCA 866
 Qy 805 ACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACT 864
 Db 867 AGGGCTGGGGGTTTCAGCCGAGCAGCGAGACTGCCGTGGCCATTCTGCGCTTCTGCAC--- 923
 Qy 865 GACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGG 924
 Db 924 -----GGCCCTGGGCTACGTCAACAGCTGCCTCAACCCCATCCTCTACGCCTTCCTGGA 977
 Qy 925 AGACCATTACA 935
 Db 978 TGAGAACTTCA 988

RESULT 8

US-09-016-434-1391

; Sequence 1391, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g471316
US-09-016-434-1391

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Query Match          5.3%; Score 82.2; DB 4; Length 1973;
Best Local Similarity 44.5%; Pred. No. 3.7e-13;
Matches 379; Conservative 0; Mismatches 463; Indels 9; Gaps 1;

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Qy      85 GGCTATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACT 144
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Db      315 GCCCCTCGGGCTCAAGGTCACCATCGTGGGGCTCTACCTGGCCGTGTGTGTCGGAGGGCT 374

Qy      145 GCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAG 204
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Db      375 CCTGGGGAAGTGCCTTGTCATGTACGTATCCTCAGGCACACCAAATGAAGACAGCCAC 434

Qy      205 CAATGTCTATCTTTTAAACCTTTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCAT 264
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Db      435 CAATATTTACATCTTTAAACCTGGCCCTGGCCGACACTCTGGTCCTGCTGACGCTGCCCTT 494

Qy      265 CCTGATAAAGAGTTATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAA 324
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Db      495 CCAGGGCACGGACATCCTCCTGGGCTTCTGGCCGTTTGGGAATGCGCTGTGCAAGACAGT 554

Qy      325 CCGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCAT 384
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      555 CATTGCCATTGACTACTACAACATGTTACCAGCACCTTCACCCTAAGTCCCATGAGTGT 614

Qy      385 GGACCGATATCTGCTCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATT 444
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Db      615 GGATCGCTATGTAGCCATCTGCCACCCATCCGTGCCCTCGACGTCCGCACGTCCAGCAA 674

Qy      445 TGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCT 504
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      675 AGCCCAGGCTGTCAATGTGGCCATCTGGGCCCTGGCCTCTGTTGTCGGTGTTCCTGGTGC 734

Qy      505 CACTTTCATCAATTCTGTCCCAAAAGAAGAGGGGAGTAAGTGCATCGACTATGCAAGTTC 564
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Db 735 CATCATGGGCTCGGCACAGGTCGAGGATGAAGAGATCGAGTGCCTGGTGGAGATCCCTAC 794
 Qy 565 TGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAAT 624
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 Db 795 CCCTCAGGATTACTGGGGCCCCGGTGTTCGCCATCTGCATCTTCCTCTCTCCTTCATCGT 854
 Qy 625 TCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAG 684
 | | | | | | | | | | | | | | | | | |
 Db 855 CCCCCTGCTCGTCATCTCTGTCTGCTACAGCCTCATGATCCGGCGGCTCCGTGGAGTCCG 914
 Qy 685 CCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGT 744
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 Db 915 CCTGCTCTCGGGCTCCCGAGAGAAGGACCGGAACCTGCGGCGCATCACTCGGCTGGTGCT 974
 Qy 745 TGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTC 804
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 Db 975 GGTGGTAGTGGCTGTGTTTCGTGGGCTGCTGGACGCCTGTCCAGGTCTTCGTGCTGGCCCA 1034
 Qy 805 ACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACT 864
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 Db 1035 AGGGCTGGGGGTTTCAGCCGAGCAGCGAGACTGCCGTGGCCATTCGCGCTTCTGCAC--- 1091
 Qy 865 GACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGG 924
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 Db 1092 -----GGCCCTGGGCTACGTCAACAGCTGCCTCAACCCCATCCTCTACGCCTTCCTGGA 1145
 Qy 925 AGACCATTACA 935
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 Db 1146 TGAGAACTTCA 1156

RESULT 9

US-08-461-244-1

; Sequence 1, Application US/08461244

; Patent No. 5776729

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,244

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; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1586 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 431..1495
US-08-461-244-1

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Query Match          5.2%; Score 80; DB 1; Length 1586;
Best Local Similarity 47.3%; Pred. No. 1.4e-12;
Matches 276; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

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Qy      98 AAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTC 157
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Db      533 AAGTTGCTCCTTGCTGTCTTTTATTGCCTCCTGTTTGTATTTCAGTCTTCTGGGAAACAGC 592

Qy      158 ACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTT 217
      ||  |  |  |  |  |  |||||  ||||  |||  ||  ||  ||||  ||  ||
Db      593 CTGGTCATCCTGGTCCTTGTGGTCTGCAAGAAGCTGAGGAGCATCACAGATGTATACCTC 652

Qy      218 TTAAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGT 277
      ||  |||||  ||  |  |||||  |  |||  |  |  |  |  |  |  |  |
Db      653 TTGAACCTGGCCCTGTCTGACCTGCTTTTTGTCTTCTCCTTCCCCTTTTCAGACCTA---C 709

Qy      278 TATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTT 337
      |||  ||  ||  ||  |  |||  |||  |  ||  |  |  |  |  |  |
Db      710 TATCTGCTGGACCAAGTGGGTGTTTGGGACTGTAATGTGCAAAGTGGTGTCTGGCTTTTAT 769

Qy      338 CACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTG 397
      |||  |  |||||  |||||  |  ||  ||||  ||||  ||  ||||  |  ||  |||
Db      770 TACATTGGCTTCTACAGCAGCATGTTTTTCATCACCTCATGAGTGTGGACAGGTACCTG 829

Qy      398 CTCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATC 457
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      830 GCTGTTGTCCATGCCGTGTATGCCCTAAAGGTGAGGACGATCAGGATGGGCACAACGCTG 889

Qy      458 TCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAAT 517
      |  |||||  ||  |||  |  |  |  |  |  |  |  ||  ||||  ||  ||  |
Db      890 TGCCTGGCAGTATGGCTAACC GCCATTATGGCTACCATCCCATTGCTAGTGT'TTTACCAA 949

Qy      518 TCTGTCCCAAAGAAGAGGGCAGTAAGTGCATCGACTATGCAAGTTCTGGAAACCCTGAA 577
      |  |  |  ||||  |  |  |  ||  |  |  |  |  |  |  |
Db      950 GTGGCCTCTGAAGATGGTGTCTACAGTGTATTTCATTTTACAATCAACAGACTTTGAAG 1009

```

Qy 578 CACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTG 637
 || || | || | || || | || || || | || | || |
 Db 1010 TGGAAGATCTTCACCAACTTCAAATGAACATTTTAGGCTTGTTGATCCCATTACCATC 1069

Qy 638 ATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAG 681
 | ||| ||| || || | | |||| |
 Db 1070 TTTATGTTCTGCTACATTAAATCCTGCACCAGCTGAAGAGGTG 1113

RESULT 10

US-09-016-434-1096

; Sequence 1096, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1096:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1953 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g1245056

US-09-016-434-1096

Query Match 5.2%; Score 80; DB 4; Length 1953;
 Best Local Similarity 47.3%; Pred. No. 1.5e-12;
 Matches 276; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

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Qy      98 AAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTC 157
      ||| | | | | | | | | | | | | | | | | | | | |
Db      369 AAGTTGCTCCTTGCTGTCTTTTATTGCCTCCTGTTTGTATTTCAGTCTTCTGGGAAACAGC 428

Qy      158 ACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTT 217
      || | | | | | | | | | | | | | | | | | | | |
Db      429 CTGGTCATCCTGGTCCTTGTGGTCTGCAAGAAGCTGAGGAGCATCACAGATGTATACCTC 488

Qy      218 TTTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGT 277
      || | | | | | | | | | | | | | | | | | | | |
Db      489 TTGAACCTGGCCCTGTCTGACCTGCTTTTTTGTCTTCTCCTTCCCCTTTCAGACCTA---C 545

Qy      278 TATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTT 337
      ||| | | | | | | | | | | | | | | | | | |
Db      546 TATCTGCTGGACAGTGGGTGTTTGGGACTGTAATGTGCAAAGTGGTGTCTGGCTTTTAT 605

Qy      338 CACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTG 397
      ||| | | | | | | | | | | | | | | | | | |
Db      606 TACATTGGCTTCTACAGCAGCATGTTTTTCATCACCCTCATGAGTGTGGACAGGTACCTG 665

Qy      398 CTCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATC 457
      | | | | | | | | | | | | | | | | | | | |
Db      666 GCTGTTGTCCATGCCGTGTATGCCCTAAAGGTGAGGACGATCAGGATGGGCACAACGCTG 725

Qy      458 TCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAAT 517
      | | | | | | | | | | | | | | | | | | | |
Db      726 TGCCTGGCAGTATGGCTAACGCCATTATGGCTACCATCCCATTGCTAGTGTTTTACCAA 785

Qy      518 TCTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAA 577
      | | | | | | | | | | | | | | | | | | | |
Db      786 GTGGCCTCTGAAGATGGTGTCTACAGTGTATTTCATTTTACAATCAACAGACTTTGAAG 845

Qy      578 CACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTG 637
      || | | | | | | | | | | | | | | | | | | |
Db      846 TGGAAGATCTTCACCAACTTCAAATGAACATTTTAGGCTTGTGTATCCCATTCACCATC 905

Qy      638 ATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAG 681
      | | | | | | | | | | | | | | | | | | | |
Db      906 TTTATGTTCTGCTACATTAAATCCTGCACCAGCTGAAGAGGTG 949
  
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RESULT 11

US-08-513-974B-57

; Sequence 57, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-513-974B-57

Query Match 5.2%; Score 79.6; DB 3; Length 984;
Best Local Similarity 46.0%; Pred. No. 1.4e-12;
Matches 388; Conservative 0; Mismatches 444; Indels 12; Gaps 3;

Qy	89	ATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTT	148
Db	67	AACTTCAAGCAACTGCTGCTGCCACCTGTGTATTTCGGCGGTGCTGGCGGCTGGCCTGCCG	126
Qy	149	GGGAATGTCACCTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAAT	208
Db	127	CTGAACATCTGTGTCATTACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCC	186
Qy	209	GTCTATCTTTTTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCCTTCCCATCCTG	268
Db	187	GTGTACACCCTAAACCTTGCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCTGCTC	246
Qy	269	ATAAAGAGTTATGCCAA---TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAAC	325
Db	247	ATCTACAACATATGCCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCTGGTC	306
Qy	326	CGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATG	385
Db	307	CGCTTCCTCTTCTATGCCAACCTGCACGGCAGCATCCTCTTCCTCACTGCATCAGCTTC	366
Qy	386	GACCGATATCTGCTCATGAAGTACCCTTT---CCGAGAACACTTCTACAAAAGAAGGAA	442
Db	367	CAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCCGCCGG	426
Qy	443	TTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATG	502
Db	427	GCTGCCTGGCTAGTGTGTGTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCACA	486
Qy	503	CTCACTTTCATCAATTCTGTCCCAAAAGAAGAGGGCAGTAACCTGCATCGACTATGCAAGT	562
Db	487	GCCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCG	546
Qy	563	TCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTA	622
Db	547	CCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTG	606
Qy	623	ATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGG	682
Db	607	CTGCCCTTTGCTGCCCTGCTGGCCTGCTACTGTCTCCTGGCCTGCCGCTGTGCCGCCAG	666
Qy	683	AGCCAGCAGCAAGCAACTG-----CCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC	736
Db	667	GATGGCCCGGCAGAGCCTGTGGCCAGGAGCGGCGTGGCAAGGCGGCCGCGATGGCCGTG	726

Qy 737 CTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG 796
 ||| ||| || ||| | || ||| ||| ||| |
 Db 727 GTGGTGGCTGCTGCCTTTGCCATCAGCTTCCTGCCTTTTCACATCACCAAGACAGCCTAC 786
 Qy 797 ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA 856
 | || || | | | | | | | | | | | |
 Db 787 CTGGCAGTGGGCTCGACGCCGGGCGTCCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCC 846
 Qy 857 TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC 916
 |||| | || |||| | || | |||| | | |||| || || |
 Db 847 TACAAAGGCACGCGGCCGTTTGCCAGTGCCAACAGCGTGCTGGACCCCATCCTCTTCTAC 906
 Qy 917 CTCA 920
 |||
 Db 907 TTCA 910

RESULT 12

US-09-461-436B-57

; Sequence 57, Application US/09461436B

; Patent No. 6538107

; GENERAL INFORMATION:

; APPLICANT: Shuji Hinuma

; Yasuaki Ito

; Ryo Fujii

; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
 ; Production, And Use Thereof

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwards & Angell, LLP

; STREET: 101 Federal Street

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02209

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/461,436B

; FILING DATE: 14-Dec-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/513,974

; FILING DATE: 14-SEP-1995

; APPLICATION NUMBER: PCT/JP95/01599

; FILING DATE: 10-AUG-1995

; APPLICATION NUMBER: 7-093989

; FILING DATE: 19-APR-1995

; APPLICATION NUMBER: 7-057186

; FILING DATE: 16-MAR-1995

; APPLICATION NUMBER: 7-007177

; FILING DATE: 20-JAN-1995

; APPLICATION NUMBER: 6-326611

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; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-461-436B-57

```

```

Query Match          5.2%; Score 79.6; DB 4; Length 984;
Best Local Similarity 46.0%; Pred. No. 1.4e-12;
Matches 388; Conservative 0; Mismatches 444; Indels 12; Gaps 3;

```

```

Qy      89 ATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTT 148
      | ||| || | | || | | ||| | | | | ||| |||
Db      67 AACTTCAAGCAACTGCTGCTGCCACCTGTGTATTGCGCGGTGCTGGCGGCTGGCCTGCCG 126

Qy      149 GGAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAAT 208
      ||| || ||| | | | | | | | | | | | | |||
Db      127 CTGAACATCTGTGTCATTACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCC 186

Qy      209 GTCTATCTTTTAAACCTTTCCATCTCTGACTTTGCTTTTCCTGTGCACCCTTCCCATCCTG 268
      || || | ||||| | | |||| | | | ||| ||| ||| |||
Db      187 GTGTACACCCTAAACCTTGCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCTGCTC 246

Qy      269 ATAAAGAGTTATGCCAA---TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAAC 325
      || | | ||||| | ||| | || ||| ||| || | |||
Db      247 ATCTACAACATATGCCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCTGCCGCTGGTC 306

Qy      326 CGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATG 385
      || | | | | ||||| || ||||| ||||| ||||| ||| |||
Db      307 CGCTTCCTCTTCTATGCCAACCTGCACGGCAGCATCCTCTTCCTCACCTGCATCAGCTTC 366

Qy      386 GACCGATATCTGCTCATGAAGTACCCTTT---CCGAGAACACTTTCTACAAAAGAAGGAA 442
      | || || ||| ||| |||| | || ||| |
Db      367 CAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCCGCCGG 426

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Qy 443 TTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATG 502
 |||| | | | | | | | | | | | | | | | |
 Db 427 GCTGCCTGGCTAGTGTGTGTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCCACA 486

Qy 503 CTCAC'TTTCATCAATTCTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGT 562
 || ||| | | | | | | | | | | | | |
 Db 487 GCCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCG 546

Qy 563 TCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTA 622
 ||| | | | | | | | | | | | | | | | | |
 Db 547 CCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTG 606

Qy 623 ATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGG 682
 | | | | | | | | | | | | | | | | | | | |
 Db 607 CTGCCCTTTGCTGCCCTGCTGGCCTGCTACTGTCTCCTGGCCTGCCGCCTGTGCCGCCAG 666

Qy 683 AGCCAGCAGCAAGCAACTG-----CCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC 736
 | | | | | | | | | | | | | | | | | | | |
 Db 667 GATGGCCCGGCAGAGCCTGTGGCCAGGAGCGGCGTGGCAAGGCGGCCCGCATGGCCGTG 726

Qy 737 CTGGCGGTGTGTATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG 796
 ||| || | | | | | | | | | | | | | | | |
 Db 727 GTGGTGGCTGCTGCCTTTGCCATCAGCTTCCTGCCTTTTCACATCACCAAGACAGCCTAC 786

Qy 797 ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA 856
 | | | | | | | | | | | | | | | | | | | |
 Db 787 CTGGCAGTGGGCTCGACGCCGGGCGTCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCC 846

Qy 857 TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC 916
 |||| | | | | | | | | | | | | | | | | | |
 Db 847 TACAAAGGCACGCGGCCGTTTGCCAGTGCCAAACAGCGTGTGGACCCCATCCTCTTCTAC 906

Qy 917 CTCA 920
 |||
 Db 907 TTCA 910

RESULT 13

US-08-513-974B-379

; Sequence 379, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA
;
; ZIP: 02109
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/513,974B
;
; FILING DATE: 14-SEP-1995
;
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/JP95/01599
;
; FILING DATE: 10-AUG-1995
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 7-093989
;
; FILING DATE: 19-AUG-1995
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 7-057186
;
; FILING DATE: 16-MAR-1995
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 7-007177
;
; FILING DATE: 20-JAN-1995
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-326611
;
; FILING DATE: 28-DEC-1994
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-270017
;
; FILING DATE: 02-NOV-1994
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-236357
;
; FILING DATE: 30-SEP-1994
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-236356
;
; FILING DATE: 30-SEP-1994
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-189274
;
; FILING DATE: 11-AUG-1994
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-189273
;
; FILING DATE: 11-AUG-1945
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 6-189272
;
; FILING DATE: 11-AUG-1994
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Resnick, David S.
;
; REGISTRATION NUMBER: 34,235
;
; REFERENCE/DOCKET NUMBER: 45753
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 617-523-3400
;
; TELEFAX: 617-523-6440
;
; INFORMATION FOR SEQ ID NO: 379:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1023 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..1020
US-08-513-974B-379

Query Match 5.2%; Score 79.6; DB 3; Length 1023;
Best Local Similarity 46.0%; Pred. No. 1.4e-12;
Matches 388; Conservative 0; Mismatches 444; Indels 12; Gaps 3;

Qy 89 ATCTTGAATAAGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTT 148
| ||| || | || | | ||| | | | ||| |||
Db 103 AACTTCAAGCAACTGCTGCTGCCACCTGTGTATTCGGCGGTGCTGGCGGCTGGCCTGCCG 162

Qy 149 GGAATGTCACTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAAT 208
||| || ||| | | | | | | | ||| |||
Db 163 CTGAACATCTGTGTCAATTACCCAGATCTGCACGTCCCGCCGGGCCCTGACCCGCACGGCC 222

Qy 209 GTCTATCTTTTTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTG 268
|| || | ||||| | | ||||| | | ||| ||| ||| |||
Db 223 GTGTACACCCTAAACCTTGCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCTGCTC 282

Qy 269 ATAAAGAGTTATGCCAA---TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAAC 325
|| | | ||||| | |||| | |||| ||| | | |||
Db 283 ATCTACAACTATGCCCAAGGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCCTGGTC 342

Qy 326 CGATATGTGCTTCACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATG 385
|| | | | | ||||| || ||||| ||||| ||| ||| |
Db 343 CGCTTCCTCTTCTATGCCAACCTGCACGGCAGCATCCTCTTCCTCACCTGCATCAGCTTC 402

Qy 386 GACCGATATCTGCTCATGAAGTACCCTTT---CCGAGAACACTTTCTACAAAAGAAGGAA 442
| ||| ||| ||| |||| | || ||| |
Db 403 CAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCCGCCGG 462

Qy 443 TTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATG 502
|||| ||| | | | |||| |||| | || ||||
Db 463 GCTGCCTGGCTAGTGTGTGTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCACA 522

Qy 503 CTCACCTTTCATCAATTCTGTCCCAAAAGAAGAGGGCAGTAAGTGCATCGACTATGCAAGT 562
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Db 523 GCCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCCG 582

Qy 563 TCTGGAAACCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTA 622
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Db 583 CCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCACTGTCATCGGCTTCCTG 642

Qy 623 ATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGG 682
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Db 643 CTGCCCTTTGCTGCCCTGCTGGCCTGCTACTGTCTCCTGGCCTGCCGCCTGTGCCGCCAG 702

Qy 683 AGCCAGCAGCAAGCAACTG-----CCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC 736
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Db 703 GATGGCCCGGCAGAGCCTGTGGCCCAGGAGCGGCGTGGCAAGGCGGCCCGCATGGCCGTG 762

Qy 737 CTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG 796
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Db 763 GTGGTGGCTGCTGCCTTTGCCATCAGCTTCCTGCCTTTTCACATCACCAAGACAGCCTAC 822


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Qy      797 ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA 856
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Db      823 CTGGCAGTGGGCTCGACGCCGGGCGTCCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCC 882

Qy      857 TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC 916
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Db      883 TACAAAGGCACGCGGCCGTTTGCCAGTGCCAACAGCGTGCTGGACCCCATCCTCTTCTAC 942

Qy      917 CTCA 920
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Db      943 TTCA 946

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RESULT 14

US-08-432-174A-3

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; Sequence 3, Application US/08432174A
; Patent No. 6562587
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, BRIGITTE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
; TITLE OF INVENTION: NUCLEIC ACIDS CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: EX92009-US
; CURRENT APPLICATION NUMBER: US/08/432,174A
; CURRENT FILING DATE: 1995-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
; NAME/KEY: modified_base
; LOCATION: (922)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (927)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (931)..(932)
; OTHER INFORMATION: a, t, c, g, other or unknown

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US-08-432-174A-3

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Query Match          5.1%; Score 79.2; DB 4; Length 998;
Best Local Similarity 50.0%; Pred. No. 1.8e-12;
Matches 198; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy      166 GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCT 225
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Db      93 GTTCGGCATCGTCCGGTACACTAAGATGAAGACGACCACCAAGATCTACATCTTCAACCT 152

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Qy 226 TTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAA 285
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 Db 153 GGCCTTAGCCGATGCGCTGGCCACCAGCACGCTGCCTTCCAGAGTGCCAAGTACCTGAT 212
 Qy 286 TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAA 345
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 Db 213 GGAGACGTGGCCCTTCGGCGAGCTGCTCTGCAAGGCTGTGCTCTCCATCGACTACTACAA 272
 Qy 346 CCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAA 405
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 Db 273 TATGTTACCAGCATCTTCACGCTCACCATGATGAGTGTGACCGCTACATCGCTGTCTG 332
 Qy 406 GTACCCTTTCGAGAACACTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGC 465
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 Db 333 CCACCCTGTCAAGGCCCTGGACTTCCGCACGCCTGCCAAGGCCAAGCTGATCAACATCTG 392
 Qy 466 TGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCAT 501
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 Db 393 TATCTGGGTCTTGGCCTCAGGCGTTGGCGTGCCCAT 428

RESULT 15

US-09-016-434-1190

; Sequence 1190, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

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; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1495 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179984
US-09-016-434-1190
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Query Match          5.1%; Score 78.4; DB 4; Length 1495;
Best Local Similarity 54.1%; Pred. No. 3.8e-12;
Matches 160; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
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Job time : 107 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 15:00:25 ; Search time 516 Seconds
(without alignments)
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Perfect score: 1543
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1543	100.0	1543	11	US-09-891-138A-1	Sequence 1, Appli
2	592.4	38.4	1005	13	US-10-272-983-35	Sequence 35, Appl
3	592.4	38.4	1005	13	US-10-393-807-35	Sequence 35, Appl
4	592.4	38.4	1380	15	US-10-225-567A-566	Sequence 566, App
5	592.4	38.4	1436	13	US-09-764-886-36	Sequence 36, Appl
6	592.4	38.4	4232	13	US-09-764-886-11	Sequence 11, Appl
7	590.8	38.3	1428	15	US-10-270-587-1	Sequence 1, Appli
8	126.6	8.2	1014	9	US-09-943-798-3	Sequence 3, Appli
9	126.6	8.2	1014	11	US-09-885-453-2	Sequence 2, Appli
10	126.6	8.2	1014	13	US-10-321-807-27	Sequence 27, Appl
11	126.6	8.2	1014	15	US-10-270-144-1	Sequence 1, Appli
12	126.6	8.2	1014	15	US-10-188-405-7	Sequence 7, Appli
13	126.6	8.2	1014	15	US-10-079-384-13	Sequence 13, Appl
14	126.6	8.2	1014	15	US-10-225-567A-646	Sequence 646, App
15	126.6	8.2	1081	13	US-10-010-568-1	Sequence 1, Appli
16	126.6	8.2	1414	13	US-10-017-161-525	Sequence 525, App
17	126.6	8.2	9905	15	US-10-270-144-3	Sequence 3, Appli
18	125	8.1	1014	13	US-10-278-141-10	Sequence 10, Appl
19	125	8.1	1014	13	US-10-296-081-10	Sequence 10, Appl
20	125	8.1	1014	15	US-10-023-775B-1	Sequence 1, Appli
21	119.2	7.7	1020	11	US-09-782-974C-85	Sequence 85, Appl
22	119	7.7	1313	10	US-09-728-422-1	Sequence 1, Appli
23	104	6.7	1020	13	US-10-023-586B-3	Sequence 3, Appli
24	100.8	6.5	2424	15	US-10-225-567A-218	Sequence 218, App
25	97.8	6.3	1002	13	US-10-088-726-25	Sequence 25, Appl
26	97.8	6.3	1082	13	US-10-023-586B-1	Sequence 1, Appli
27	97.8	6.3	1334	13	US-10-017-161-707	Sequence 707, App
28	97.8	6.3	3143	13	US-10-275-910-1	Sequence 1, Appli
29	96	6.2	831	9	US-09-943-798-1	Sequence 1, Appli
30	95.4	6.2	1017	11	US-09-885-453-3	Sequence 3, Appli
31	95.4	6.2	1017	15	US-10-079-384-5	Sequence 5, Appli
32	90	5.8	1651	13	US-10-366-288-41	Sequence 41, Appl
33	88.4	5.7	1098	15	US-10-225-567A-331	Sequence 331, App
34	88.4	5.7	1429	11	US-09-077-173A-1	Sequence 1, Appli
35	87	5.6	2118	13	US-10-101-510-431	Sequence 431, App
36	85.4	5.5	2025	13	US-10-101-510-722	Sequence 722, App
37	85.4	5.5	2025	15	US-10-225-567A-216	Sequence 216, App
38	84.8	5.5	2796	13	US-10-024-298A-173	Sequence 173, App
39	84.8	5.5	2796	13	US-10-042-211A-173	Sequence 173, App
40	83.8	5.4	1113	13	US-09-826-509-540	Sequence 540, App
41	83	5.4	850	13	US-10-275-910-4	Sequence 4, Appli
42	83	5.4	851	13	US-10-275-910-6	Sequence 6, Appli
43	82.8	5.4	1571	13	US-10-354-358-9	Sequence 9, Appli
44	82.8	5.4	1832	15	US-10-225-567A-222	Sequence 222, App
45	82.2	5.3	1805	9	US-09-823-114-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-891-138A-1

; Sequence 1, Application US/09891138A

; Publication No. US20030083245A1

; GENERAL INFORMATION:

; APPLICANT: Lin, Daniel Chi-Hong

; APPLICANT: Zhao, Jiagang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030083245A1e1 Receptors
 ; FILE REFERENCE: 018781-006210US
 ; CURRENT APPLICATION NUMBER: US/09/891,138A
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIOR APPLICATION NUMBER: US 60/213,461
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1543
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (44)..(997)
 ; OTHER INFORMATION: mouse TGR18 G-protein coupled receptor (GPCR)
 US-09-891-138A-1

Query Match 100.0%; Score 1543; DB11; Length 1543;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA	120
Db	61	TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA	120
Qy	121	TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACGTGGTGTTCGGCTACCTCTT	180
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Db	181	CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTAACCTTTCCATCTCTGACTT	240
Qy	241	TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA	300
Db	241	TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA	300
Qy	301	TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT	360
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Qy	361	CCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCCGAGA	420
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Qy	421	ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCCTTAGT	480
Db	421	ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCCTTAGT	480

Qy	481	GACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGGGCAG	540
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Qy	661	GGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACC	720
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Qy	1021	CAGCCAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTAACTAAGTAAACC	1080
Db	1021	CAGCCAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTAACTAAGTAAACC	1080
Qy	1081	ACCATTTCTAGGCTTTAGCTTTCCACCATCCTCCAACCCCAGGGCTGGAGTACAAGCTG	1140
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Qy	1141	GGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGG	1200
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Qy	1201	AAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACA	1260
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Qy	1261	AATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGGAAATTTTAAGACCTCTTTT	1320
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 Qy 1501 ATTTCTTGAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543
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RESULT 2

US-10-272-983-35

; Sequence 35, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/272,983
 ; CURRENT FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: US/09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 1005
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-272-983-35

Query Match 38.4%; Score 592.4; DB 13; Length 1005;
Best Local Similarity 75.5%; Pred. No. 2.1e-138;
Matches 750; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

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Db      8 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 67

Qy     99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     68 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 127

Qy    159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    128 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 187

Qy    219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    188 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 247

Qy    279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    248 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 307

Qy    339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    308 ATGCCAACCTCTATACCAGCATTCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA 367

Qy    399 TCATGAAGTACCCTTTCCGAGAACACCTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    368 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 427

Qy    459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    428 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 487

Qy    519 CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAACCCCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    488 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 547

Qy    579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    548 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 607

Qy    639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    608 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 667

Qy    699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCCTGGCGGTTGTGATCTTCTCTA 758
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    668 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 727

Qy    759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    728 TGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 787
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; ORGANISM: Homo sapiens
US-10-393-807-35

Query Match 38.4%; Score 592.4; DB 13; Length 1005;
Best Local Similarity 75.5%; Pred. No. 2.1e-138;
Matches 750; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      8 GGATCATGGCATGGAATGCAACTTGCAAAAAGCTGGCTGGCAGCAGAGGCTGCCCTGGAAA 67

Qy     99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     68 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 127

Qy    159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    128 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 187

Qy    219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    188 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 247

Qy    279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    248 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 307

Qy    339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    308 ATGCCAACCTCTATACCAGCATCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA 367

Qy    399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    368 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 427

Qy    459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    428 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 487

Qy    519 CTGTCCCAAAAGAAGAGGGCAGTAAGTGCATCGACTATGCAAGTTCTGGAAACCCCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    488 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAGTTCTGGAGACCCCAACT 547

Qy    579 ACAATCTCATTTACAGCCTCTGCCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    548 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 607

Qy    639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    608 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 667

Qy    699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA 758
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    668 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 727

Qy    759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy	39	GCAGAATGGCACAGAAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA	98
Db	50	GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA	109
Qy	99	AGTACTACCTCTCTGCATTTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA	158
Db	110	AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA	169
Qy	159	CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT	218

Db	170	TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT	229
Qy	219	TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT	278
Db	230	TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT	289
Qy	279	ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC	338
Db	290	ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC	349
Qy	339	ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC	398
Db	350	ATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA	409
Qy	399	TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT	458
Db	410	TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT	469
Qy	459	CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT	518
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Qy	519	CTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAAC	578
Db	530	CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCACT	589
Qy	579	ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA	638
Db	590	ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTTCCTTATTCCTCTTTTTGTGA	649
Qy	639	TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA	698
Db	650	TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA	709
Qy	699	CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA	758
Db	710	CTGCTCTGCCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG	769
Qy	759	TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT	818
Db	770	TGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT	829
Qy	819	G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC	875
Db	830	GGAAGCAGTATCAGTGCACCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT	889
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA	935
Db	890	TGGCCTTTCTGAACAGTGTCAATCAACCCTGTCTTCTATTTTCTTTTGGGAGATCACTTCA	949
Qy	936	GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT	995
Db	950	GGGACATGCTGATGAATCAACTGAGACACAACCTTCAAATCCCTTACATCCTTTAGCAGAT	1009
Qy	996	GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG	1048
Db	1010	GGGCTCATGAACCTCTACTTTTCATTGAGAGAAAAGTGAGGGGCTTGTGAAACAG	1063

RESULT 5

US-09-764-886-36

; Sequence 36, Application US/09764886

; Publication No. US20030139327A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ02

; CURRENT APPLICATION NUMBER: US/09/764,886

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 1436

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-886-36

Query Match 38.4%; Score 592.4; DB 13; Length 1436;

Best Local Similarity 75.3%; Pred. No. 2.6e-138;

Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      100 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 159

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      160 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCCTGGAAATACCA 219

Qy      159 CTGTGGTGTTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      220 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 279

Qy      219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
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Db      280 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 339

Qy      279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      340 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 399

Qy      339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACCTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      400 ATGCCAACCTCTATACCAGCATTCCTTTCTCACCTTTTATCAGCATAGATCGATACTTGA 459

Qy      399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      460 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 519

Qy      459 CGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      520 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 579

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Qy 519 CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAAC 578
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 Db 580 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 639
 Qy 579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
 |||| ||||| |||| | || || || ||||| |||| | |||||
 Db 640 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 699
 Qy 639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
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 Db 700 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 759
 Qy 699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA 758
 |||| |||| || || || || | |||| || |||| || || |||||
 Db 760 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 819
 Qy 759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
 | || || ||||| ||||| || ||||| ||||| ||||| |||||
 Db 820 TGCTTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 879
 Qy 819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
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 Db 880 GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT 939
 Qy 876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA 935
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 Db 940 TGGCCTTTCTGAACAGTGTCTCAACCCTGTCTTCTATTTTCTTTTGGGAGATCACTTCA 999
 Qy 936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
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 Db 1000 GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT 1059
 Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
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 Db 1060 GGGCTCATGAACTCCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTGTGAAACAG 1113

RESULT 6

US-09-764-886-11

; Sequence 11, Application US/09764886
 ; Publication No. US20030139327A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ02
 ; CURRENT APPLICATION NUMBER: US/09/764,886
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 4232
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-886-11

Query Match 38.4%; Score 592.4; DB 13; Length 4232;

Best Local Similarity 75.3%; Pred. No. 5.1e-138;
Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     110 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 169

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     170 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGAAATACCA 229

Qy     159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     230 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 289

Qy     219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     290 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 349

Qy     279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     350 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 409

Qy     339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
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Db     410 ATGCCAACCTCTATACCAGCATTCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA 469

Qy     399 TCATGAAGTACCCTTTCCGAGAACACTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
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Db     470 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAGAAAGAGTTTGCTATTTTAATCT 529

Qy     459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     530 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 589

Qy     519 CTGTCCCAAAAGAAGAGGGCAGTAAGTGCATCGACTATGCAAGTTCTGGAAACCCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     590 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 649

Qy     579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     650 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 709

Qy     639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     710 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAGGTTGCTA 769

Qy     699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA 758
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     770 CTGCTCTGCCCTTGAAAAGCCTCTCAACTGGTCATCATGGCAGTGGAATCTTCTCTG 829

Qy     759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     830 TGCTTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 889

Qy     819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
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Db 890 GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT 949
 Qy 876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA 935
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 Db 950 TGGCCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTTTGGGAGATCATTCA 1009
 Qy 936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
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 Db 1010 GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT 1069
 Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
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 Db 1070 GGGCTCATGAACTCCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTTGTGAAACAG 1123

RESULT 7

US-10-270-587-1

; Sequence 1, Application US/10270587

; Publication No. US20030054487A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; TITLE OF INVENTION: Human G-Protein Coupled Receptor

; FILE REFERENCE: PF217C2

; CURRENT APPLICATION NUMBER: US/10/270,587

; CURRENT FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: US 09/908,593

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 08/781,456

; PRIOR FILING DATE: 1997-01-10

; PRIOR APPLICATION NUMBER: US 60/009,902

; PRIOR FILING DATE: 1996-01-11

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1428

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-270-587-1

Query Match 38.3%; Score 590.8; DB 15; Length 1428;

Best Local Similarity 75.2%; Pred. No. 6.7e-138;

Matches 763; Conservative 0; Mismatches 247; Indels 4; Gaps 2;

Qy 39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
 | | ||||| |||| | |||| | || || ||||| ||||| | || | |
 Db 99 GGATCATGGCATGGAATGCAACTTGCAAAAAGTGGCTGGCAGCAGAGGCTGCCCTGGAAA 158
 Qy 99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158
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 Db 159 AGTACTACCTTTCCATTTTATGGGATTGAGTTCGTTGTGGGAGTTCCTTGGAATACCA 218
 Qy 159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
 ||| || | ||||| ||||| ||||| ||||| ||||| ||| | ||||| |
 Db 219 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 278
 Qy 219 TTAACCTTTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
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Db 279 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 338

Qy 279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
 ||||| || ||| ||||| || |||| | ||||| ||||| |||||

Db 339 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 398

Qy 339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
 | ||||| ||||| ||||| ||||| || |||| | |||| |

Db 399 ATGCCAACCTCTATACCAGCATTCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA 458

Qy 399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
 | || |||| | |||| | |||| | |||| | |||| | || || |||||

Db 459 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAAGAAAGAGTGTGCTATTTTAATCT 518

Qy 459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
 | |||| | |||| |||| | |||| | |||| | || | || ||||

Db 519 CCTTGGCCATGTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 578

Qy 519 CTGTCCCAAAAGAAGAGGGCAGTAACCTGCATCGACTATGCAAGTTCTGGAAACCCTGAAC 578
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Db 579 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 638

Qy 579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
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Db 639 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 698

Qy 639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
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Db 699 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 758

Qy 699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA 758
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Db 759 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 818

Qy 759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
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Db 819 TGCTTTTTACACCCTATCACGTATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 878

Qy 819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
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Db 879 GGAAGCAGTATCAGTGCCTCAGGTCGTCACTCACTCCTTTTACATTGTGACACGGCCTG 938

Qy 876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA 935
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Db 939 TGGCCTTTCTGAACAGTGTCAACCTGTCTTCTATTTTCTTGTGGGAGATCACTTCA 998

Qy 936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
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Db 999 GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT 1058

Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAA-TGAGACACTTGATAAACAG 1048
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Db 1059 GGGCTCATGAACTCCTACTTTTCATTAGAGAAAAGTGAGGGGCTTGTGAAACAG 1112

; Sequence 3, Application US/09943798
 ; Patent No. US20020065215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glaxo Group Limited
 ; TITLE OF INVENTION: Polypeptide
 ; FILE REFERENCE: QG1021
 ; CURRENT APPLICATION NUMBER: US/09/943,798
 ; CURRENT FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-943-798-3

Query Match 8.2%; Score 126.6; DB 9; Length 1014;
 Best Local Similarity 49.9%; Pred. No. 3e-21;
 Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

Qy	60	CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT	119
Db	59	CTTTTGGAAATTGCACTGATGAAAACATCCCCTCAAGATGCACTACCTCCCTGTTATTT	118
Qy	120	ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCT	179
Db	119	ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT	178
Qy	180	TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACT	239
Db	179	TCAAAATGAGACCTTGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC	238
Qy	240	TTGCTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA	296
Db	239	TGCTGTATCTGACCAGCCTCCCCTTCTGATTCACTACTATGCCAGTGGCGAAACTGGA	298
Qy	297	CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA	356
Db	299	TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA	358
Qy	357	GCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC	416
Db	359	GCATCCTCTTCCTCACCTGTTTCAGCATCTTCGCTACTGTGTGATCATTACCCAATGA	418
Qy	417	GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAACTCTCGCTGGCTGTCTGGGCCT	476
Db	419	GCTGCTTTTCCATTACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA	478
Qy	477	TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGG	536
Db	479	TTTCACTGGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA	538
Qy	537	GCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCC	596
Db	539	GATCAGCCTGTCTCGACCTCACCAGTTCGG-----ATGAACCAATACTATTAAGTGGT	592
Qy	597	TCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA	656

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Db      593 ACAACCTGATTTTGGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCT 652
Qy      657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
      | | | | | | | | | | | | | | | | | | | | | |
Db      653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACCTGACAGCTGCCTTAAGCAGA 712
Qy      717 AACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
      | | | | | | | | | | | | | | | | | | | | | |
Db      713 AAGCACGAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTACCCTTCC 772
Qy      777 ATATCATGCGCAATTTGAGGATCGCCTCACGCCTG 811
      | | | | | | | | | | | | | | | | | | | | | |
Db      773 ATATCTTGAGGGTCATTTCGGATCGAATCTCGCCTG 807

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RESULT 9

US-09-885-453-2

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; Sequence 2, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRx10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA nucleotide sequence
; LOCATION: (1)..(1014)
; OTHER INFORMATION: GPCRx10 DNA sequence
US-09-885-453-2

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Query Match          8.2%; Score 126.6; DB 11; Length 1014;
Best Local Similarity 49.9%; Pred. No. 3e-21;
Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

```

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Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      | | | | | | | | | | | | | | | | | | | | | |
Db      59 CTTTTGGAAATTGCACTGATGAAAACATCCCCTCAAGATGCACTACCTCCCTGTTATTT 118
Qy      120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCT 179
      | | | | | | | | | | | | | | | | | | | | | |
Db      119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178
Qy      180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCTTTCCATCTCTGACT 239
      | | | | | | | | | | | | | | | | | | | | | |
Db      179 TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 238
Qy      240 TTGCTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296

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Db      239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298

Qy      297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
      || ||||| | | ||| | ||| | | ||||| || | ||
Db      299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGCA 358

Qy      357 GCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
      ||||| ||||| | | |||| | || | | || | |
Db      359 GCATCCTCTTCCTCACCTGTTTCAGCATCTCCGCTACTGTGTGATCATTACCCCAATGA 418

Qy      417 GAGAACAACCTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCT 476
      |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      419 GCTGCTTTTCCATTACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478

Qy      477 TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGG 536
      |   ||| || | || || | | |||| | | | | |
Db      479 TTTCACTGGTAGCTGTCACTCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA 538

Qy      537 GCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCC 596
      |   ||| |||| | |||| | | |||| |||| ||| | |
Db      539 GATCAGCCTGTCTCGACCTCACCAGTTCGG-----ATGAACTCAATACTATTAAGTGGT 592

Qy      597 TCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA 656
      |   |||| |||| | | | | | ||| | || | | | |
Db      593 ACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCT 652

Qy      657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
      || | | | | | | | | | | |||| | | | | |
Db      653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACCTGACAGCTGCCTTAAGCAGA 712

Qy      717 AACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
      || | | | | | | ||| | | | || | || | |||| |
Db      713 AAGCACGAAGGCTAACCATTCTGCTACTCCTTGCAATTTTACGTATGTTTTTTACCCCTCC 772

Qy      777 ATATCATGCGCAATTTGAGGATCGCCTCACGCCTG 811
      ||||| || | | ||||| || |||||
Db      773 ATATCTTGAGGGTCATTCGGATCGAATCTCGCCTG 807

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RESULT 10

US-10-321-807-27

; Sequence 27, Application US/10321807

; Publication No. US20030166148A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Rupong

; APPLICANT: Dang, Huong T.

; APPLICANT: Lowitz, Kevin P.

; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G Protein-Coupled

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN0086

; CURRENT APPLICATION NUMBER: US/10/321,807

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US/09/714,008

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/170,496

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; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-27

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```

Query Match          8.2%; Score 126.6; DB 13; Length 1014;
Best Local Similarity 49.9%; Pred. No. 3e-21;
Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

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Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      ||| || ||||| | | | | | | | | | | | | | | |
Db      59 CTTTTGGAAATTGCACTGATGAAAACATCCCACCTCAAGATGCACTACCTCCCTGTTATTT 118

Qy     120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCT 179
      ||| || ||| | | ||| | | || |||| | | | | | | | |
Db     119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178

Qy     180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCTTTCCATCTCTGACT 239
      || |||| | |||| ||||| | | | | | | | | | | | |
Db     179 TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 238

Qy     240 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
      | | | | ||| ||| ||| ||||| | | ||||| | | ||| |||
Db     239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAACTGGA 298

Qy     297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
      || ||||| | | |||| | ||| | | || | ||||| || | ||
Db     299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCATTTCACCTGTATAGCA 358

Qy     357 GCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
      ||||| ||||| ||| | |||| | ||| | | || | |||| |
Db     359 GCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGA 418

Qy     417 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAAATCTCGCTGGCTGTCTGGGCCT 476
      | | | | ||| | ||| ||| ||| | | ||| ||| |
Db     419 GCTGCTTTTCCATTACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478

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; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1el Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR164
US-10-188-405-7

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Query Match          8.2%; Score 126.6; DB 15; Length 1014;
Best Local Similarity 49.9%; Pred. No. 3e-21;
Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

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Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      ||| || ||||| | | | | | ||| ||| |||
Db      59 CTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 118

Qy     120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCAGTGTGGTGTTCGGCTACCTCT 179
      ||| || ||| | | ||| | | || ||| ||| | | ||| | |
Db     119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178

Qy     180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACT 239
      || |||| |||| ||||| || | | | |||| || | | ||
Db     179 TCAAAATGAGACCTTGAAGAGCAGCACCATCATATGCTGAACCTGGCCTGCACAGATC 238

Qy     240 TTGCTTTCTCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
      | | | || || || || ||||| | . ||||| | || || |||
Db     239 TGCTGTATCTGACCAGCCTCCCCTTCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298

Qy     297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
      || ||||| | | |||| | ||| | | || ||||| || | ||
Db     299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGTATAGCA 358

Qy     357 GCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
      ||||| ||||| || | |||| || || | || | |||| |
Db     359 GCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCAATGA 418

Qy     417 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCT 476
      | | | || || | || || | || || | || || || |
Db     419 GCTGCTTTTCCATTACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478

Qy     477 TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCCAAAAGAAGAGG 536
      | ||| || || || || | || |||| || | | | |
Db     479 TTTCACTGGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA 538

Qy     537 GCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCC 596
      | ||| |||| | |||| | |||| |||| ||| | |
Db     539 GATCAGCCTGTCTCGACCTCACCAGTTCGG-----ATGAACCAATACTATTAAGTGGT 592

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Qy 597 TCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA 656
 | | | | | | | | | | | | | | | | | | | | | |
 Db 593 ACAACCTGATTTTGACTGCAACTACTTTCTGCCCTCCCCTTGGTGATAGTGACACTTTGCT 652
 Qy 657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
 | | | | | | | | | | | | | | | | | | | | | |
 Db 653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACCTGACAGCTGCCCTAAGCAGA 712
 Qy 717 AACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
 | | | | | | | | | | | | | | | | | | | | | |
 Db 713 AAGCACGAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTTACCCTTCC 772
 Qy 777 ATATCATGCGCAATTTGAGGATCGCCTCACGCCTG 811
 | | | | | | | | | | | | | | | | | | | | | |
 Db 773 ATATCTTGAGGGTCATTTCGGATCGAATCTCGCCTG 807

RESULT 13

US-10-079-384-13

; Sequence 13, Application US/10079384

; Publication No. US20030108986A1

; GENERAL INFORMATION:

; APPLICANT: Communi, Didier

; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: 9409/2132

; CURRENT APPLICATION NUMBER: US/10/079,384

; CURRENT FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 09/885,453

; PRIOR FILING DATE: 2001-06-20

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1014)

; OTHER INFORMATION:

US-10-079-384-13

Query Match 8.2%; Score 126.6; DB 15; Length 1014;

Best Local Similarity 49.9%; Pred. No. 3e-21;

Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

Qy 60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
 | | | | | | | | | | | | | | | | | | | | | |
 Db 59 CTTTGGAAATTGCACTGATGAAACATCCCCTCAAGATGCACTACCTCCCTGTTATTT 118
 Qy 120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCT 179
 | | | | | | | | | | | | | | | | | | | | | |
 Db 119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178
 Qy 180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTAACCTTTCCATCTCTGACT 239
 | | | | | | | | | | | | | | | | | | | | | |

; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 646
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-646

Query Match 8.2%; Score 126.6; DB 15; Length 1014;
Best Local Similarity 49.9%; Pred. No. 3e-21;
Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

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Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      ||| || ||||| | | | | | | | | | | | | | |
Db      59 CTTTTGGAAATTGCACTGATGAAAACATCCCCTCAAGATGCACTACCTCCCTGTTATTT 118

Qy     120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCT 179
      ||| || ||| | | ||| | | || |||| | | | | | | | |
Db     119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178

Qy     180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACT 239
      || |||| | |||| ||||| || | | | |||| | | ||
Db     179 TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATC 238

Qy     240 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
      | | | ||| || ||| ||| ||||| | | ||||| | | || |||
Db     239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298

Qy     297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
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RESULT 15

US-10-010-568-1

; Sequence 1, Application US/10010568

; Publication No. US20030157598A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM23,
EXPRESSED HIGHLY IN

; TITLE OF INVENTION: KIDNEY

FILE REFERENCE: D0077 NP

; CURRENT APPLICATION NUMBER: US/10/010,568

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/251,926

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/269,795

; PRIOR FILING DATE: 2001-02-14

; NUMBER OF SEQ ID NOS: 55

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; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 1

; LENGTH: 1081

; TYPE: DNA

; ORGANISM: homo sapiens

; FEATURE:

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; NAME/KEY: CDS
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; LOCATION: (54)..(1064)

US-10-010-568-1

Query Match 8.2%; Score 126.6; DB 13; Length 1081;

Best Local Similarity 49.9%; Pred. No. 3.1e-21;

Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

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Qy 120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGAATGTCACGTGGTGTTTCGGCTACCTCT 179

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Qy 180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCTTTCCATCTCTGACT 239

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Qy 240 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296

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Search completed: December 14, 2003, 17:43:01
 Job time : 519 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 11:13:44 ; Search time 5878 Seconds
(without alignments)
10738.951 Million cell updates/sec

Title: US-09-891-138A-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	5	645.8	41.9	60298	2	AC116149	AC116149 Mus muscu
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c	7	615.8	39.9	326606	2	AC110839	AC110839 Rattus no
	8	592.4	38.4	1325	9	AF247785	AF247785 Homo sapi
	9	592.4	38.4	1380	6	AX549281	AX549281 Sequence
	10	592.4	38.4	1380	9	AF348078	AF348078 Homo sapi
	11	592.4	38.4	1449	9	BC030948	BC030948 Homo sapi
	12	592.4	38.4	1542	6	AX342665	AX342665 Sequence
	13	590.2	38.3	90343	9	AC116026	AC116026 Homo sapi
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	19	145.2	9.4	69462	2	AC101335	AC101335 Mus muscu
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	21	126.6	8.2	1014	6	AX148186	AX148186 Sequence
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ALIGNMENTS

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LOCUS AX376573 1543 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 1 from Patent WO0200719.

ACCESSION AX376573

VERSION AX376573.1 GI:19170674

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Lin,D.C., Zhao,J., Chen,J.L. and Cutler,G.

TITLE Novel receptors

JOURNAL Patent: WO 0200719-A 1 03-JAN-2002;
Tularik Inc. (US)

FEATURES Location/Qualifiers

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CDS 44..997
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BASE COUNT 438 a 352 c 293 g 460 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA	120
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Db	121	 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTTCGGCTACCTCTT	180
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RESULT 2

AF295367

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DEFINITION Mus musculus G-protein coupled receptor GPR91 mRNA, complete cds.
ACCESSION  AF295367
VERSION    AF295367.1  GI:12711490
KEYWORDS   .
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1598)

AUTHORS Wittenberger,T., Schaller,H.C. and Hellebrand,S.

TITLE An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors

JOURNAL J. Mol. Biol. 307 (3), 799-813 (2001)

MEDLINE 21172992

PUBMED 11273702

REFERENCE 2 (bases 1 to 1598)

AUTHORS Wittenberger,T., Schaller,C.H. and Hellebrand,S.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2000) ZMNH, Institut fur Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany

FEATURES Location/Qualifiers

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CDS 74. .1027

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Best Local Similarity 99.6%; Pred. No. 0;

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Db	331	TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT	390
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Db	391	GCTCTTGCTCACTGTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCCGAGA	450
Qy	421	ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGT	480
Db	451	ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGT	510
Qy	481	GACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCCAAAAGAAGAGGGCAG	540
Db	511	GACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCCAAAAGAAGAGGGCAG	570
Qy	541	TAACTGCATCGACTATGCAAGTTCTGGAAACCTGAACACAATCTCATTTACAGCCTCTG	600
Db	571	TAACTGCATCGACTATGCAAGTTCTGGAAACCTGAACACAATCTCATTTACAGCCTCTG	630
Qy	601	CCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGAT	660
Db	631	CCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGAT	690
Qy	661	GGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACC	720
Db	691	GGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACC	750
Qy	721	CCAACGCCTGGTGGTCTGGCGGTGTGATCTTCTCTATACTCTTCACACCCTATCATAT	780
Db	751	CCAACGCCTGGTGGTCTGGCAGTTGTGATCTTCTCTATACTCTTCACACCCTATCATAT	810
Qy	781	CATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAA	840
Db	811	CATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAA	870
Qy	841	GGCCATCAAATCTATATACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAA	900
Db	871	GGCCATCAAATCTATATACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAA	930
Qy	901	TCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAG	960
Db	931	TCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAG	990
Qy	961	ACAATACTTCAAGTCCCTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACT	1020
Db	991	ACAATACTTCAAGTCCCTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACT	1050
Qy	1021	CAGCCAAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTAACTAAGTAAACC	1080
Db	1051	CAGCCAAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTAACTAAGTAAACC	1110
Qy	1081	ACCATTTCTAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTG	1140
Db	1111	ACCATTTCTAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTG	1170

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 Db 1171 GGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGG 1230

Qy 1201 AAAAAATAAGGCATGAGAAAGCATTTGACATCTTCACTTAAGAACTGAACAAAAGAGAACA 1260
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 Db 1471 TTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTTCTATTTGAAAATTAT 1530

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 Db 1531 ATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1573

RESULT 3

AC138318/c

LOCUS AC138318 184306 bp DNA linear HTG 22-MAR-2003

DEFINITION Mus musculus chromosome 3 clone RP23-358I23 map 3, WORKING DRAFT
 SEQUENCE, 10 unordered pieces.

ACCESSION AC138318

VERSION AC138318.3 GI:29150501

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 184306)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Mus musculus chromosome 3, clone RP23-358I23

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 184306)

AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
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 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (25-DEC-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 184306)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
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 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
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 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Mar 22, 2003 this sequence version replaced gi:28191615.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L28921
 Center clone name: 358_I_23
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 181695 bases at least Q40
 Consensus quality: 182410 bases at least Q30
 Consensus quality: 182638 bases at least Q20
 Insert size: 170000; agarose-fp
 Insert size: 183406; sum-of-contigs
 Quality coverage: 12.8 in Q20 bases; agarose-fp
 Quality coverage: 11.9 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 58928: contig of 58928 bp in length
 * 58929 59028: gap of 100 bp
 * 59029 59675: contig of 647 bp in length
 * 59676 59775: gap of 100 bp
 * 59776 64745: contig of 4970 bp in length
 * 64746 64845: gap of 100 bp
 * 64846 69474: contig of 4629 bp in length
 * 69475 69574: gap of 100 bp
 * 69575 73672: contig of 4098 bp in length
 * 73673 73772: gap of 100 bp
 * 73773 81217: contig of 7445 bp in length
 * 81218 81317: gap of 100 bp
 * 81318 97238: contig of 15921 bp in length
 * 97239 97338: gap of 100 bp
 * 97339 113368: contig of 16030 bp in length
 * 113369 113468: gap of 100 bp
 * 113469 166137: contig of 52669 bp in length
 * 166138 166237: gap of 100 bp
 * 166238 184306: contig of 18069 bp in length.

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misc_feature	59776. .64745 /note="assembly_fragment"
misc_feature	64846. .69474 /note="assembly_fragment"
misc_feature	69575. .73672 /note="assembly_fragment"
misc_feature	73773. .81217 /note="assembly_fragment"
misc_feature	81318. .97238 /note="assembly_fragment"
misc_feature	97339. .113368 /note="assembly_fragment"
misc_feature	113469. .166137 /note="assembly_fragment"


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misc_feature      166238. .184306
                  /note="assembly_fragment
                  clone_end:T7
                  vector_side:right"
BASE COUNT      58167 a  34380 c  35771 g  55088 t    900 others
ORIGIN

Query Match      96.9%; Score 1494.8; DB 2; Length 184306;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      46 GGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTA 105
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Db      145736 GGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTA
145677

Qy      106 CCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCACTGTGGT 165
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Db      145676 CCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCACTGTGGT
145617

Qy      166 GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCT 225
          |||
Db      145616 GTTTGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCT
145557

Qy      226 TTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAA 285
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Db      145556 TTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAA
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Qy      286 TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAA 345
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Db      145436 CCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAA
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Db      145316 TGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCC
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Db      145256 AAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAACACAATCT
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Qy	766		CACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACA	825
Db	145016		CACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACA	
	144957			
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Db 144416 AATGCATTTTCATCATTGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTATTTTTATT
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Qy 1426 CTTGTAATATTAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTT 1485
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Db 144356 CTTGTAATATTAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTT
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Qy 1486 CTATTTGAAATTATATTTCTTGAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543
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RESULT 4

AC111231/c

LOCUS AC111231 239576 bp DNA linear HTG 13-MAY-2003

DEFINITION Rattus norvegicus clone CH230-96013, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.

ACCESSION AC111231

VERSION AC111231.7 GI:30578486

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 239576)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,

Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
 Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
 Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
 Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
 Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
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 Morgan,M., Morris,K., Morris,S., Munidas,M., Murphy,M., Nair,L.,
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 Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
 Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
 Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
 Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
 Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
 Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 239576)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 239576)
 AUTHORS Rat Genome Sequencing Consortium.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On May 13, 2003 this sequence version replaced gi:24819079.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Qy	46	GGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTA	105
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Qy	106	CCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGT	165
Db	92514	CCTCTCTGCATTTTATGGGATCGAGTTCATTGTTGGAATGCTTGGCAATTACCGTGGT	92455
Qy	166	GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACT	225
Db	92454	GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGTAGCAACGTCTATCTTCAACT	92395

Qy 226 TTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAA 285
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 Db 92394 TTCCATCTCTGACCTTGCTTTTCTGTGCACGCTTCCCATGCTGATAAGGAGTTACGCCAC 92335

Qy 286 TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAA 345
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Qy 346 CCTCTACACCAGCATCCTCTTCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAA 405
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Qy 406 GTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGC 465
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 Db 92214 GTTCCCTTTCCGAGAACACATTCTACAAAAGAAGGAATTTGCCATTTTAATCTCCCTGGC 92155

Qy 466 TGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCC 525
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Qy 526 AAAAGAAGAGGGCAGTAACCTGCATCGACTATGCAAGTTCTGGAAACCTGAACACAATCT 585
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 Db 92094 AATAGAAAAGGGCGACAGCTGTGTGACTATGCAAGTTCTGGAAACCTAAATACAGTCT 92035

Qy 586 CATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTT 645
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Qy 706 GCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTATACTCTT 765
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 Qy 1304 ATTTTAAGACCTCTT-TTTCTATCAGTGTAAGGAATACAAGATAGCTAGTTGCAATG 1362
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 Qy 1534 AATCAATATA 1543
 Db 91091 AATCAACACA 91082

RESULT 5

AC116149

LOCUS AC116149 60298 bp DNA linear HTG 25-MAR-2002

DEFINITION Mus musculus clone RP24-540E9, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC116149

VERSION AC116149.1 GI:19703273

KEYWORDS HTG; HTGS PHASE0.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 60298)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Mus musculus, clone RP24-540E9

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 60298)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (25-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24912
 Center clone name: 540_E_9

 * NOTE: This record contains 77 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
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 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.
 * 1 656: contig of 656 bp in length
 * 657 756: gap of 100 bp
 * 757 1426: contig of 670 bp in length
 * 1427 1526: gap of 100 bp
 * 1527 2210: contig of 684 bp in length
 * 2211 2310: gap of 100 bp
 * 2311 2997: contig of 687 bp in length
 * 2998 3097: gap of 100 bp
 * 3098 3786: contig of 689 bp in length
 * 3787 3886: gap of 100 bp
 * 3887 4577: contig of 691 bp in length
 * 4578 4677: gap of 100 bp
 * 4678 5357: contig of 680 bp in length
 * 5358 5457: gap of 100 bp

*	5458	6150: contig of 693 bp in length
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*	6251	6817: contig of 567 bp in length
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*	7716	8412: contig of 697 bp in length
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Query Match 41.9%; Score 645.8; DB 2; Length 60298;
Best Local Similarity 84.0%; Pred. No. 2.4e-133;
Matches 673; Conservative 0; Mismatches 127; Indels 1; Gaps 1;

Qy	51	AGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCT	110
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Db	4609	NN	4668
Qy	831	GTACACAGAAGGCCATCAAAT	851
Db	4669	NNNNNNNNNCGGAGATCTGAT	4689

Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L24912
Center clone name: 540_E_9

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* 43737 43836: gap of 100 bp
* 43837 44525: contig of 689 bp in length
* 44526 44625: gap of 100 bp
* 44626 45306: contig of 681 bp in length
* 45307 45406: gap of 100 bp
* 45407 46111: contig of 705 bp in length
* 46112 46211: gap of 100 bp
* 46212 46848: contig of 637 bp in length
* 46849 46948: gap of 100 bp
* 46949 47639: contig of 691 bp in length
* 47640 47739: gap of 100 bp
* 47740 48431: contig of 692 bp in length
* 48432 48531: gap of 100 bp
* 48532 49221: contig of 690 bp in length
* 49222 49321: gap of 100 bp
* 49322 50017: contig of 696 bp in length
* 50018 50117: gap of 100 bp
* 50118 50799: contig of 682 bp in length
* 50800 50899: gap of 100 bp
* 50900 51583: contig of 684 bp in length
* 51584 51683: gap of 100 bp
* 51684 52384: contig of 701 bp in length
* 52385 52484: gap of 100 bp
* 52485 53167: contig of 683 bp in length
* 53168 53267: gap of 100 bp
* 53268 53966: contig of 699 bp in length
* 53967 54066: gap of 100 bp

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Query Match          41.1%;  Score 633.6;  DB 2;  Length 60298;
Best Local Similarity 97.6%;  Pred. No. 1.2e-130;
Matches 664;  Conservative 0;  Mismatches 14;  Indels 2;  Gaps 2;

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Qy      379 TAGCATGGACCGATATCTGCTCATGAAGTACCCTTCCGAG-AACACTTTCTACAAAA-G 436
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Db      36659 TAGCATGGACCGATATCTGCTCATGAAGTACCCTTCCGAGAAACACTTTCTACAAAANG 36600
          |||
Qy      437 AAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTA 496
          |||

```

Db 36599 AAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCTTTAGTGACCTTAGAAGTTCTA 36540
 Qy 497 CCCATGCTCACTTTTCATCAATTCTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTAT 556
 |||||
 Db 36539 CCCATGCTCACTTTTCATCAATTCTGTCCCAAAGAAGAGGGCAGTAACTGCATCGACTAT 36480
 Qy 557 GCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGC 616
 |||||
 Db 36479 GCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGC 36420
 Qy 617 TTCCTAATTCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAG 676
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 Db 36419 TTCCTAATTCTCTCTCTGTGATGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAG 36360
 Qy 677 AGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC 736
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 Db 36359 AGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTC 36300
 Qy 737 CTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG 796
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 Db 36299 CTGGCAGTTGTGATCTTCTCTATACTCTTCACACCCTATCATATCATGCGCAATTTGAGG 36240
 Qy 797 ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA 856
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 Db 36239 ATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAAGGCCATCAAATCTATA 36180
 Qy 857 TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC 916
 |||||
 Db 36179 TACACACTGACACGGCCTCTGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTC 36120
 Qy 917 CTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCC 976
 |||||
 Db 36119 CTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCC 36060
 Qy 977 CTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAATGAGACA 1036
 |||||
 Db 36059 CTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAATGAGACA 36000
 Qy 1037 CTTGATAAACAGTGCTGTGC 1056
 || | || | ||
 Db 35999 CTGAGAATCCACCACAGGGC 35980

RESULT 7

AC110839/c

LOCUS AC110839 326606 bp DNA linear HTG 11-OCT-2002

DEFINITION Rattus norvegicus clone CH230-208A12, *** SEQUENCING IN PROGRESS
 ***, 25 unordered pieces.

ACCESSION AC110839

VERSION AC110839.4 GI:23820318

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 326606)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 326606)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 326606)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Oct 11, 2002 this sequence version replaced gi:21739250. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRKD

Center clone name: CH230-208A12

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 242752 bases at least Q40

Consensus quality: 250821 bases at least Q30

Consensus quality: 254983 bases at least Q20

Estimated insert size: 244968; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 25 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 10356: contig of 10356 bp in length

* 10357 10456: gap of unknown length

* 10457 15819: contig of 5363 bp in length

* 15820 15919: gap of unknown length

* 15920 245368: contig of 229449 bp in length

* 245369 245468: gap of unknown length

* 245469 272041: contig of 26573 bp in length

* 272042 272141: gap of unknown length

* 272142 276368: contig of 4227 bp in length

* 276369 276468: gap of unknown length

* 276469 282159: contig of 5691 bp in length

* 282160 282259: gap of unknown length

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* 282260 283432: contig of 1173 bp in length
* 283433 283532: gap of unknown length
* 283533 284633: contig of 1101 bp in length
* 284634 284733: gap of unknown length
* 284734 285764: contig of 1031 bp in length
* 285765 285864: gap of unknown length
* 285865 287082: contig of 1218 bp in length
* 287083 287182: gap of unknown length
* 287183 288399: contig of 1217 bp in length
* 288400 288499: gap of unknown length
* 288500 289828: contig of 1329 bp in length
* 289829 289928: gap of unknown length
* 289929 291274: contig of 1346 bp in length
* 291275 291374: gap of unknown length
* 291375 293018: contig of 1644 bp in length
* 293019 293118: gap of unknown length
* 293119 294732: contig of 1614 bp in length
* 294733 294832: gap of unknown length
* 294833 296078: contig of 1246 bp in length
* 296079 296178: gap of unknown length
* 296179 297942: contig of 1764 bp in length
* 297943 298042: gap of unknown length
* 298043 299812: contig of 1770 bp in length
* 299813 299912: gap of unknown length
* 299913 301595: contig of 1683 bp in length
* 301596 301695: gap of unknown length
* 301696 304787: contig of 3092 bp in length
* 304788 304887: gap of unknown length
* 304888 306249: contig of 1362 bp in length
* 306250 306349: gap of unknown length
* 306350 307801: contig of 1452 bp in length
* 307802 307901: gap of unknown length
* 307902 309454: contig of 1553 bp in length
* 309455 309554: gap of unknown length
* 309555 314110: contig of 4556 bp in length
* 314111 314210: gap of unknown length
* 314211 326606: contig of 12396 bp in length.

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FEATURES
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                /organism="Rattus norvegicus"
                /mol_type="genomic DNA"
                /db_xref="taxon:10116"
                /clone="CH230-208A12"
    misc_feature 1. .1742
                /note="wgs_end_extension
                clone_end:Sp6"
    misc_feature complement(4245. .5082)
                /note="clone_boundary
                clone_end:Sp6
                site:EcoRI
                end_sequence:RWBKN06TVB"
    misc_feature 10457. .12850
                /note="wgs_contig"
    misc_feature 15920. .16991
                /note="wgs_contig"
    misc_feature complement(220129. .221101)
                /note="clone_boundary

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clone_end:T7
site:EcoRI
end_sequence:RWBKN06TJB"
misc_feature 241580. .242749
/note="wgs_end_extension
clone_end:T7"
misc_feature 243833. .245368
/note="wgs_end_extension
clone_end:T7"

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BASE COUNT 81699 a 50290 c 51837 g 74097 t 68683 others
ORIGIN

Query Match 39.9%; Score 615.8; DB 2; Length 326606;
Best Local Similarity 89.0%; Pred. No. 1.2e-126;
Matches 665; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Qy      46 GGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTA 105
        |||
Db      242326 GGCACAGAATTTATCTTGTGAAAATTGGCTGGCATTAGAGAATATTTTGAAAAAGTACTA
242267

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```

Qy      106 CCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCACTGTGGT 165
        |||
Db      242266 CCTCTCTGCATTTTATGGGATCGAGTTCATTTGTTGGAATGCTTGGCAATTTACCGTGGT
242207

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Qy      166 GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACT 225
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Db      242206 GTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGTAGCAACGTCTATCTTTCACT
242147

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Qy      226 TTCCATCTCTGACCTTTCCTTCTGTCACCTTCCCATCCTGATAAAGAGTTATGCCAA 285
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Db      242146 TTCCATCTCTGACCTTTCCTTCTGTCACGCTTCCCATGCTGATAAGGAGTTACGCCAC
242087

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Qy      286 TGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAA 345
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242027

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Qy      346 CCTCTACACCAGCATCCTTTCCTCACTTTTCATTAGCATGGACCGATATCTGCTCATGAA 405
        |||
Db      242026 CCTCTACACCAGCATCCTTTTCCTCACTTTTCATTAGCATAGACCGATATCTGCTCATGAA
241967

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Qy      406 GTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGC 465
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Db      241966 GTTCCCTTTCCGAGAACACATTCTACAAAAGAAGGAATTTGCCATTTTAATCTCCCTGGC
241907

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Qy      466 TGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCC 525
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Db      241906 TGTCTGGGTCTTAGTGACCTTAGAAGTTCTACCTATGCTCACGTTTATCACTTCCACCC
241847

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Qy      526 AAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCT 585

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Db      241846 AATAGAAAAGGGGCGACAGCTGTGTGCGACTATGCAAGTTCGGAAACCCTAAATACAGTCT
241787

Qy      586 CATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTT 645
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241786 CATTTACAGCCTGTGCCTGACTTTGCTGGGCTTCCTCATTCTCTGTCTGTAATGTGCTT
241727

Qy      646 CTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCT 705
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241726 CTTCTACTACAAAATGGTAGTCTTCTTAAAGAAGAGGAGCCAGCAGCAGGCAACTGTGCT
241667

Qy      706 GCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTT 765
      | ||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241666 ATCGCTGAACAAACCTCTGCGCCTGGTGGTCCTGGCAGTGGTGATCTTCTCTGTACTCTT
241607

Qy      766 CACACCCTATCATATCATGCGCAATTT 792
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241606 TACACCTTACCATATCATGCGCAATGT 241580

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RESULT 8

AF247785

LOCUS AF247785 1325 bp mRNA linear PRI 26-MAR-2002

DEFINITION Homo sapiens P2Y purinoceptor 1 mRNA, complete cds.

ACCESSION AF247785

VERSION AF247785.1 GI:19716154

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1325)

AUTHORS Zhang,W., Li,N., Wan,T. and Cao,X.

TITLE Human P2Y purinoceptor 1

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1325)

AUTHORS Zhang,W., Li,N., Wan,T. and Cao,X.

TITLE Direct Submission

JOURNAL Submitted (21-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R. China

FEATURES Location/Qualifiers

source

1. .1325

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

CDS

69. .1073

/codon_start=1

/product="P2Y purinoceptor 1"

/protein_id="AAL95690.1"

/db_xref="GI:19716155"

/translation="MLGIMAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIV
VYGYIFSLKNWNSSNIYLFNLSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVL


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      |||| |||| || || || || |   | |||| || |||| || || |||||
Db      736 CTGCTCTGCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 795

Qy      759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
      | || || ||||| ||||| ||| ||||| ||||| ||||| |||||
Db      796 TGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 855

Qy      819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
      |  || |  || || || | ||||| || | |||| | ||||| |||||
Db      856 GGAAGCAGTATCAGTGCACCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT 915

Qy      876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA 935
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Db      916 TGGCCTTTCTGAACAGTGTCAACCTGTCTTCTATTTTCTTTGGGAGATCACTTCA 975

Qy      936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
      | || ||||| || | | | |||| | ||||| ||||| ||||| || || ||
Db      976 GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT 1035

Qy      996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
      | ||| || | | |||| |||| |||| |||| |||| |||||
Db      1036 GGGCTCATGAACCTCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTTGTGAAACAG 1089

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RESULT 9

AX549281

LOCUS AX549281 1380 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 566 from Patent WO02061087.

ACCESSION AX549281

VERSION AX549281.1 GI:25813951

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides

JOURNAL Patent: WO 02061087-A 566 08-AUG-2002;
Lifespan Biosciences, Inc. (US)

FEATURES

Location/Qualifiers
source 1. .1380
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 383 a 294 c 274 g 429 t

ORIGIN

Query Match 38.4%; Score 592.4; DB 6; Length 1380;

Best Local Similarity 75.3%; Pred. No. 1.7e-121;

Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
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Db      50 GGATCATGGCATGGAATGCAACTTGCAAAAAGTGGCTGGCAGCAGAGGCTGCCCTGGAAA 109

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Qy	99	AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA	158
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Qy	159	CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT	218
Db	170		
Qy	219	TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT	278
Db	230		
Qy	279	ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC	338
Db	290		
Qy	339	ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC	398
Db	350		
Qy	399	TCATGAAGTACCCTTTCGAGAACACTTCTACAAAAGAAGGAATTTGCCATTTTAATCT	458
Db	410		
Qy	459	CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTCTACCCATGCTCACTTTCATCAATT	518
Db	470		
Qy	519	CTGTCCCAAAGAAGAGGGGAGTAAGTGCATCGACTATGCAAGTTCTGGAAACCCTGAAC	578
Db	530		
Qy	579	ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA	638
Db	590		
Qy	639	TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA	698
Db	650		
Qy	699	CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA	758
Db	710		
Qy	759	TACTCTTACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT	818
Db	770		
Qy	819	GTCTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT	878
Db	830	GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT	889
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCTCATGGGAGACCATTACA	935
Db	890		
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Qy 936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
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Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
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RESULT 12

AX342665

LOCUS AX342665 1542 bp DNA linear PAT 12-JAN-2002

DEFINITION Sequence 20 from Patent WO0198351.

ACCESSION AX342665

VERSION AX342665.1 GI:18152045

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Lal,P., Baughn,M.R., Hafalia,A.J., Nguyen,D.B., Gandhi,A.R., Kallick,D.A., Griffin,J.A., Yue,H., Khan,F.A., Patterson,C., Lu,D.A., Tribouley,C.M., Lu,Y., Walia,N.K., Graul,R., Yao,M.G., Yang,J., Ramkumar,J., Au-Young,J., Hernandez,R., Walsh,R.T. and Borowsky,M.L.

JOURNAL Patent: WO 0198351-A 20 27-DEC-2001;

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RESULT 13

AC116026

LOCUS AC116026 90343 bp DNA linear PRI 09-APR-2002

DEFINITION Homo sapiens 3 BAC RP11-3F11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

ACCESSION AC116026

VERSION AC116026.1 GI:19697319

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 90343)

AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsy,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,

Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 90343)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 90343)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence

continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

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repeat_region	complement(2568. .2741) /rpt_family="L1M4"
repeat_region	complement(2742. .3047) /rpt_family="AluSx"
repeat_region	complement(3048. .3165) /rpt_family="L1M4"
repeat_region	4735. .4865 /rpt_family="FLAM_C"
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Query Match 38.3%; Score 590.2; DB 9; Length 90343;
Best Local Similarity 75.5%; Pred. No. 6e-121;
Matches 760; Conservative 0; Mismatches 243; Indels 4; Gaps 2;

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Db     81384 TACACCCTATCACGTATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTTGGAAGCA 81443
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AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsf., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,

Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N.,
 Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N.,
 Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
 Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
 Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
 Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E.,
 Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
 Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
 Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
 Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
 Warren,R., Washington,C., Watlington,S., Williams,G.,
 Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
 Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
 Gibbs,R.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 4 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 5 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 6 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 7 (bases 1 to 132745)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Mar 28, 2002 this sequence version replaced gi:19718616.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
 gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the

entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
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repeat_region	complement(522. .1015) /rpt_family="MLT1D"
repeat_region	complement(2452. .2697) /rpt_family="L1MA5A"
repeat_region	complement(3200. .3578) /rpt_family="MLT1B"
repeat_region	3600. .3749 /rpt_family="(TA)n"
repeat_region	4391. .4411 /rpt_family="AT_rich"
repeat_region	4909. .4960

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repeat_region      complement(9359. .9460)
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repeat_region      complement(9587. .9880)
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repeat_region      complement(10203. .10450)
                   /rpt_family="L1MC4"
repeat_region      11468. .11699
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repeat_region      11717. .11886
                   /rpt_family="MLT2CB"
repeat_region      11908. .11982
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                   /rpt_family="MER8"
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                   /rpt_family="AT_rich"
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                   /rpt_family="AT_rich"
repeat_region      15465. .15739
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repeat_region      16579. .16756
                   /rpt_family="(TTATA)n"
repeat_region      complement(16757. .17074)
                   /rpt_family="L2"
repeat_region      17621. .17660
                   /rpt_family="(CAAAA)n"
repeat_region      18544. .18725

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Query Match          38.3%;  Score 590.2;  DB 9;  Length 132745;
Best Local Similarity 75.5%;  Pred. No. 6.1e-121;
Matches 760;  Conservative 0;  Mismatches 243;  Indels 4;  Gaps 2;

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Qy          46  GGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTA 105
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Db    123065  GGCATGGAATGCAACTTGCAAAAAGTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTA
123124

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Qy	106	CCTCTCTGCATTTTATGCAATCGAGTTTCATTTTTGGACTGCTTGGGAATGTCACGTGTGGT	165
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Search completed: December 14, 2003, 15:00:20
Job time : 5884 secs

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 13:14:29 ; Search time 3520 Seconds
(without alignments)
10653.922 Million cell updates/sec

Title: US-09-891-138A-1
Perfect score: 1543
Sequence: 1 gctcctggcagagttttctg.....tgccataataaatcaatata 1543

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
	No.	Score	Match	Length			
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	2	560	36.3	683	10	BB323771	BB323771 BB323771
	3	516.4	33.5	556	4	BX527630	Bx527630 RZPD Mus
	4	495.8	32.1	520	9	AI663305	AI663305 uk27c10.y
	5	455	29.5	469	10	BB744515	BB744515 BB744515
	6	438	28.4	458	10	BB746222	BB746222 BB746222
	7	414	26.8	428	10	BB738743	BB738743 BB738743
	8	403.8	26.2	422	10	BB847918	BB847918 BB847918
	9	388.4	25.2	420	10	BB864882	BB864882 BB864882
	10	384.8	24.9	426	10	BB778587	BB778587 BB778587
	11	380.4	24.7	396	10	BB739482	BB739482 BB739482
c	12	363.8	23.6	367	9	AI649254	AI649254 uk27c10.x
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	15	350.6	22.7	408	13	BY368584	BY368584 BY368584
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	17	309.8	20.1	327	10	BB220946	BB220946 BB220946
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	25	261.4	16.9	285	10	BB327439	BB327439 BB327439
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	32	214	13.9	312	10	BB498898	BB498898 BB498898
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	34	199.8	12.9	226	10	BB213317	BB213317 BB213317
c	35	192.8	12.5	956	29	CNS028Y4	AL186565 Tetraodon
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c	38	158.8	10.3	639	9	AW612141	AW612141 hg94h07.x
	39	151.2	9.8	657	13	BU352057	BU352057 603527490
	40	151	9.8	1026	29	CNS051MY	AL317059 Tetraodon
c	41	144.2	9.3	589	10	BF196066	BF196066 hr81f02.x
	42	141	9.1	1022	29	CNS04W90	AL310077 Tetraodon
c	43	139.8	9.1	582	10	BE221739	BE221739 hr58c09.x
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ALIGNMENTS

RESULT 1

AK080866

LOCUS AK080866 1585 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length /
enriched library, clone:B430012021 product:G-PROTEIN COUPLED
RECEPTOR GPR91, full insert sequence.

ACCESSION AK080866

VERSION AK080866.1 GI:26099527

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagacka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyc-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1585)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES
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ORIGIN

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Matches 1521;  Conservative 0;  Mismatches 22;  Indels 3;  Gaps 2;

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RESULT 2

BB323771

LOCUS BB323771 683 bp mRNA linear EST 31-AUG-2001

DEFINITION BB323771 RIKEN full-length enriched, 4 days neonate male adipose
Mus musculus cDNA clone B430012021 3', mRNA sequence.

ACCESSION BB323771

VERSION BB323771.2 GI:15411432

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 683)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished

COMMENT On Jul 11, 2000 this sequence version replaced gi:9032085.

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Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,
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RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source Location/Qualifiers
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTTVN 3']; cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 229.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 226 a 125 c 117 g 215 t
ORIGIN

Query Match 36.3%; Score 560; DB 10; Length 683;
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Matches 596; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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Qy 1000 TGCTGGATGCAGGTCTTCACTCAGCCAAATGAGACACTTGATAAACAGTGCTGTGCAGT 1059
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Qy	1180	TAGGTTTATACCCAGAGTATGGAAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTA	1239
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Db	666	TATA	669

RA Heil O., Ebert L., Neubert P., Peters M., Radelof U., Schneider D.,
RA Korn B.;
RT ;
RL Submitted (28-MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer
RL Feld 580, D-69120 Heidelberg, Germany

XX

CC RZPD; IMAGp998B194840.
CC RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
CC Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
CC <http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981>
CC Contact: Ina Rolfs
CC RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
CC Heubnerweg 6, D-14059 Berlin, Germany
CC Tel: +49 30 32639 101
CC Fax: +49 30 32639 111
CC www.rzpd.de
CC This clone is available royalty-free from RZPD;
CC contact RZPD (clone@rzpd.de) for further information.
CC Seq primer: sugF, Primer sequence: CTTCTGCTCTAAAAGCTGCG

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FH Key Location/Qualifiers

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FT [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
FT ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
FT cloned into distinct DraIII sites of the pME18S-FL3 vector
FT (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used
FT to isolate the cDNA insert. Size selection was performed to
FT exclude fragments <1.5kb. Library constructed by Dr. Sumio
FT Sugano (University of Tokyo Institute of Medical Science).
FT Custom primers for sequencing: 5' end primer
FT CTTCTGCTCTAAAAGCTGCG and 3' end primer
FT CGACCTGCAGCTCGAGCACA. REFERENCES: Suzuki, Y., Yoshitomo,
FT K., Maruyama, K., Suyama, A., and Sugano, S. Construction
FT and characterization of a full length-enriched and a 5' end
FT enriched cDNA library. Gene 200, 149-156, 1997. Sasaki, Z.,
FT Suzuki, Y., Watanabe, M., Imai, J., Shibui, A., Yoshida,
FT K., Hata. H., Yamaguchi, R., Tateyama, S., and Sugano, S.
FT Construction of mouse full length-enriched cDNA libraries
FT by oligo-capping. DNA Research, submitted."
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Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4

AI663305

LOCUS AI663305 520 bp mRNA linear EST 10-MAY-1999

DEFINITION uk27c10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
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ACCESSION AI663305

VERSION AI663305.1 GI:4766888

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 520)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Other_ESTs: uk27c10.x1

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 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:986966
 Seq primer: custom primer used
 High quality sequence stop: 490.

FEATURES Location/Qualifiers
 source 1. .520
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1970226"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse kidney mkia"
 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCCTACTGG]; digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
 primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 127 a 126 c 107 g 160 t
 ORIGIN

Query Match 32.1%; Score 495.8; DB 9; Length 520;
 Best Local Similarity 98.6%; Pred. No. 4.6e-92;
 Matches 500; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1  GCTCCTGGCAGAGTTTTCTGTGCGAGACAGAAGCCGACAGCAGAATGGCACAGAATTTATC 60
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Db      14 GCTCCTGGCAGAGTTTTCTGTGCGAGACAGAAGCCGACAGCTGAATGGCACAGAATTTATC 73

Qy      61 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA 120
         |||
Db      74 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA 133

Qy     121 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCTT 180
         |||
Db     134 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCTT 193

Qy     181 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTAACCTTTCCATCTCTGACTT 240
         |||
Db     194 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTAACCTTTCCATCTCTGACTT 253
  
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Qy 241 TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 300
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 Db 254 TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 313
 Qy 301 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 360
 |||
 Db 314 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 373
 Qy 361 CCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCGGAGA 420
 |||
 Db 374 GCTCTTGCTCACTGTTCATTATCATGGACCGATATCTGCTCATGAAGTACCCTGTCCGAGA 433
 Qy 421 ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGT 480
 |||
 Db 434 ACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGT 493
 Qy 481 GACCTTAGAAGTTCTACCCATGCTCAC 507
 |||
 Db 494 GACCTTAGAAGTTCTACCCATGCTCAC 520

RESULT 5

BB744515

LOCUS BB744515 469 bp mRNA linear EST_16-OCT-2001

DEFINITION BB744515 RIKEN full-length enriched, adult male kidney Mus musculus cDNA clone F530003I24 3', mRNA sequence.

ACCESSION BB744515

VERSION BB744515.1 GI:16152351

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 469)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES
source Location/Qualifiers
1. .469
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="F530003I24"
/sex="male"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, adult male kidney"
/note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTAATTAACCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. "

BASE COUNT 160 a 75 c 80 g 154 t
ORIGIN

Query Match 29.5%; Score 455; DB 10; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1089 TAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTGGGTCCACA 1148
|||||
Db 1 TAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTGGGTCCACA 60

QY 1149 TGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGGAAAAAATA 1208
|||||
Db 61 TGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGGAAAAAATA 120

Qy 1209 AGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACAAATATTGT 1268
 |||
 Db 121 AGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACAAATATTGT 180
 Qy 1269 CAATGTTTGGACACTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTTCTATCAG 1328
 |||
 Db 181 CAATGTTTGGACACTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTTCTATCAG 240
 Qy 1329 TGTAAAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGG 1388
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 Db 241 TGTAAAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGG 300
 Qy 1389 TCGATAAGCGTGTTTCTGAAATAGTCTTATTTTTATTCTTGTAATATTAAAATTTATGTG 1448
 |||
 Db 301 TCGATAAGCGTGTTTCTGAAATAGTCTTATTTTTATTCTTGTAATATTAAAATTTATGTG 360
 Qy 1449 AAAAATGAATATAAATCAATGTACAACATTAGATTTTCTATTTGAAAATTATATTTCTTG 1508
 |||
 Db 361 AAAAATGAATATAAATCAATGTACAACATTAGATTTTCTATTTGAAAATTATATTTCTTG 420
 Qy 1509 AAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543
 |||
 Db 421 AAAAAATAACTGCTGTGCCTAAATAAATCAATATA 455

RESULT 6

BB746222

LOCUS BB746222 458 bp mRNA linear EST 15-OCT-2001

DEFINITION BB746222 RIKEN full-length enriched, adult male kidney *Mus musculus* cDNA clone F530013P03 3', mRNA sequence.

ACCESSION BB746222

VERSION BB746222.1 GI:16149159

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.

REFERENCE 1 (bases 1 to 458)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
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 wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 e mouse tissues.

FEATURES Location/Qualifiers
 source 1. .458
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="F530013P03"
 /sex="male"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="SOLR"
 /clone_lib="RIKEN full-length enriched, adult male kidney"
 /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTAATTAACCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. "

BASE COUNT 150 a 75 c 82 g 151 t
 ORIGIN

Query Match 28.4%; Score 438; DB 10; Length 458;
 Best Local Similarity 99.8%; Pred. No. 4.1e-80;
 Matches 449; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1058 GTTGAGTTTAACTAAGTAAACCACCATTCTAGGCTTTAGCTTTCCACCATCCTCCAAC 1117
 |||||
 Db 10 GTTGAGTTTAACTAAGTAAACCACCATTCTAGGCTTTAGCTTTCCACCATCCTCCAAC 69

QY 1118 CCCCAGGGCTGGAGTACAAGCTGGGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGAT 1177
 |||
 Db 70 CCCCAGGGCTGGAGTACAAGCTGGGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGAT 129

QY 1178 TTTAGGTTATACCCAGAGTATGGAAAAAATAAGGCATGAGAAAGCATTGACATCTTCACT 1237
 |||
 Db 130 TTTAGGTTATACCCAGAGTATGGAAAAAATAAGGCATGAGAAAGCATTGACATCTTCACT 189

QY 1238 TAAGAACTGAACAAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATC 1297
 |||
 Db 190 TAAG-ACTGAACAAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATC 248

QY 1298 TTGGAAATTTTAAGACCTCTTTTCTATCAGTGTAAGGAATACAAGATAGCTAGTTGC 1357
 |||
 Db 249 TTGGAAATTTTAAGACCTCTTTTCTATCAGTGTAAGGAATACAAGATAGCTAGTTGC 308

QY 1358 AAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTA 1417
 |||
 Db 309 AAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTA 368

QY 1418 TTTTATTCTTGTAATATTAAATTTATGTGAAAAATGAATATAATTCAATGTACAACAT 1477
 |||
 Db 369 TTTTATTCTTGTAATATTAAATTTATGTGAAAAATGAATATAATTCAATGTACAACAT 423

QY 1478 TAGATTTTCTATTTGAAAATTATATTTCTT 1507
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 Db 429 TAGATTTTCTATTTGAAAATTATATTTCTT 458

RESULT 7

BB738743

LOCUS BB738743 428 bp mRNA linear EST 15-OCT-2001

DEFINITION BB738743 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430109C18 3', mRNA sequence.

ACCESSION BB738743

VERSION BB738743.1 GI:16141748

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 428)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

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e mouse tissues.

FEATURES

source

Location/Qualifiers

1. 428

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="F430109C18"

/tissue_type="spleen"

/dev_stage="6 days neonate"

/clone_lib="RIKEN full-length enriched, 6 days neonate spleen"

BASE COUNT 153 a 59 c 72 g 144 t
ORIGIN

Query Match 26.8%; Score 414; DB 10; Length 428;

Best Local Similarity 100.0%; Pred. No. 3.7e-75;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1130 AGTACAAGCTGGGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATAC 1189

|||||

Db 1 AGTACAACCTGGGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATAC 60

Qy 1190 CCAGAGTATGGAAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAAC 1249

|||||

Db 61 CCAGAGTATGGAAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAAC 120

Qy 1250 AAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGGAAATTTTA 1309

|||||

Db 121 AAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGGAAATTTTA 180

Qy 1310 AGACCTCTTTTCTATCAGTGTAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATG 1369

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      |||
Db      181 AGACCTCTTTTCTATCAGTGTAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATG 240
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Qy      1370 CATTTCATCATTGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTATTTTTATTCTTG 1429
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Db      241 CATTTCATCATTGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTATTTTTATTCTTG 300
      |||
Qy      1430 TAATATTAAAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTTCTAT 1489
      |||
Db      301 TAATATTAAAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTTCTAT 360
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Qy      1490 TTGAAAATTATATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543
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Db      361 TTGAAAATTATATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAATATA 414
      |||

```

RESULT 8

BB847918

LOCUS BB847918 422 bp mRNA linear EST 26-NOV-2001

DEFINITION BB847918 RIKEN full-length enriched, adult male kidney Mus musculus cDNA clone F530201F11 5', mRNA sequence.

ACCESSION BB847918

VERSION BB847918.1 GI:17086293

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 422)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

181 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTTAACCTTTCCATCTCTGACTT 240

Db 196 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACTT 255
 Qy 241 TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 300
 Db 256 TGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 315
 Qy 301 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 360
 Db 316 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 375
 Qy 361 CCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAAGT 407
 Db 376 CCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGGTCATGAAGT 422

RESULT 9

BB864882

LOCUS BB864882 420 bp mRNA linear EST 27-NOV-2001

DEFINITION BB864882 RIKEN full-length enriched, RCB-1283 B16 melanoma cDNA Mus musculus cDNA clone G430047C11 5', mRNA sequence.

ACCESSION BB864882

VERSION BB864882.1 GI:17111092

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 420)

AUTHORS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES Location/Qualifiers
 source 1. .420
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="G430047C11"
 /cell_line="RCB-1283 B16 melanoma"
 /clone_lib="RIKEN full-length enriched, RCB-1283 B16 melanoma cDNA"

BASE COUNT 102 a 103 c 87 g 128 t
ORIGIN

Query Match 25.2%; Score 388.4; DB 10; Length 420;
Best Local Similarity 99.5%; Pred. No. 7.3e-70;
Matches 400; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY      1 GCTCCTGGCAGAGTTTTCTGTGCGAGACAGAAGCCGACAGCAGAATGGCACAGAATTATC 60
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Db      19 GCTCCTGGCAGAGTTTTCTGTGCGAGACAGAAGCCGACAGCAGAATGGCACAGAATTATC 78

QY      61 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA 120
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Db      79 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA 138

QY     121 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCTT 180
      |||
Db     139 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCTT 198

QY     181 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACTT 240
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Db     199 CTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACTT 258

QY     241 TGCTTTCTGTGCACCCTTCCCATCTTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 300
      |||
Db     259 TGCTTTCTGTGCACCCTTCCCATCTTGATAAAGAGTTATGCCAATGATAAGGGGACCTA 318

QY     301 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 360
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Db     319 TGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCAGCAT 378

QY     361 CCTCTTCCTCACTTTTCATTAG-CATGGACCGATATCTGCTCA 401
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Db     379 CCTCTTCCTCACTTTTCATTAGCCATGGACCGATATCTGCTCA 420
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RESULT 10

BB778587

LOCUS BB778587 426 bp mRNA linear EST 15-NOV-2001

DEFINITION BB778587 RIKEN full-length enriched, RCB-1283 B16 melanoma cDNA Mus musculus cDNA clone G430047C11 3', mRNA sequence.

ACCESSION BB778587

VERSION BB778587.1 GI:16939287

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 426)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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URL: <http://genome.gsc.riken.go.jp/>

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

Location/Qualifiers

SOURCE

1. 426

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"
/clone="G430047C11"
/cell_line="RCB-1283 B16 melanoma"
/clone_lib="RIKEN full-length enriched, RCB-1283 B16
melanoma cDNA"

BASE COUNT 153 a 58 c 76 g 139 t
ORIGIN

Query Match 24.9%; Score 384.8; DB 10; Length 426;
Best Local Similarity 98.8%; Pred. No. 4.1e-69;
Matches 419; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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Qy      1123 GGGCTGGAGTACAAGCTGGGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAG 1182
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Qy      1183 GTTATACCCAGAGTATGGAAAAAATAA-GGCATGAGAAAGCATTGACATCTTCACTTAAG 1241
          |||
Db       63 GTTATACCCAGAGTATGGAAAAAATAAGGGCATGAAAAAGCATTGACATCTTCACTTAAG 122

Qy      1242 AACTGAACAAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGG 1301
          |||
Db       123 AACTGAACAAAAGAGAACAAATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTTG 182

Qy      1302 AAATTTTAAGACCTCTTTTTCTATCAGTGTA AAAAGGAATACAAGATAGCTAGTTGCAAAT 1361
          |||
Db       183 AAATTTTAAGACCTCTTTTTCTATCAGTGTA AAAAGGAATACAAGATAGCTAGTTGCAAAT 242

Qy      1362 GCTGAATGCATTTCATCATTGGTCA-3GTCGATAAGCGTGTTTCTGAAATAGTCTTATTT 1420
          |||
Db       243 GCTGAATGCATTTCATCATTGGTCAAGCGTGTTTCTGAAATAGTCTTATTT 302

Qy      1421 TTATTCTTGTAATATTAAAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAG 1480
          |||
Db       303 TTATTCTTGTAATATTAAAAATTTATGTGAAAAATGAATATAATTCAATGTACAACATTAG 362

Qy      1481 ATTTTCTA-TTTGAAAATTATATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAA 1539
          |||
Db       363 ATTTCTAGTTTGAAAATTATATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAA 422

Qy      1540 TATA 1543
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Db       423 TATA 426
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RESULT 11

BB739482

LOCUS BB739482 396 bp mRNA linear EST 15-OCT-2001

DEFINITION BB739482 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F430113M16 3', mRNA sequence.

ACCESSION BB739482

VERSION BB739482.1 GI:16142487

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 396)
 AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
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 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 e mouse tissues.

FEATURES Location/Qualifiers
 source 1. .396
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="F430113M16"
 /tissue_type="spleen"
 /dev_stage="6 days neonate"
 /clone_lib="RIKEN full-length enriched, 6 days neonate spleen"

BASE COUNT 142 a 52 c 62 g 140 t
 ORIGIN

Query Match 24.7%; Score 380.4; DB 10; Length 396;
 Best Local Similarity 99.7%; Pred. No. 3.3e-68;

Matches 381; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1162 AGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGGAAAAAATAAGGCATGAGAAAG 1221
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Qy      1222 CATTGACATCTTCACCTTAAGAACTGAACAAAAGAGAACAAATATTGTCAATGTTTGGACA 1281
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Qy      1282 CTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTTCTATCAGTGTAAGGAATA 1341
          |||
Db      121  CTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTTCTATCAGTGTAAGGAATA 180

Qy      1342 CAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATAAGCGTGT 1401
          |||
Db      181  CAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATAAGCGTGT 240

Qy      1402 TTCTGAAATAGTCTTATTTTATTCTTGTAATATTTAAATTTATGTGAAAAATGAATATA 1461
          |||
Db      241  TTCTGAAATAGTCTTATTTTATTCTTGTAATATTTAAATTTATGTGAAAAATGAATATA 300

Qy      1462 ATTCAATGTACAACATTAGATTTTCTATTTGAAAATTATATTTCTTGAAAAATAACTGC 1521
          |||
Db      301  ATTCAATTTACAACATTAGATTTTCTATTTGAAAATTATATTTCTTGAAAAATAACTGC 360

Qy      1522 TGTGCCTAAATAAATCAATATA 1543
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Db      361  TGTGCCTAAATAAATCAATATA 382
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RESULT 12

AI649254/c

LOCUS AI649254 367 bp mRNA linear EST 30-APR-1999

DEFINITION uk27c10.x1 Sugano mouse kidney mkoa Mus musculus cDNA clone

IMAGE:1970226 3', mRNA sequence.

ACCESSION AI649254

VERSION AI649254.1 GI:4730088

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 367)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Other ESTs: uk27c10.y1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:986966

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end

Seq primer: custom primer used

High quality sequence stop: 353.

FEATURES

source

Location/Qualifiers

1. .367

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1970226"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Sugano mouse kidney mkia"

/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

BASE COUNT

106 a 73 c 71 g 117 t

ORIGIN

Query Match 23.6%; Score 363.8; DB 9; Length 367;
Best Local Similarity 99.5%; Pred. No. 8.9e-65;
Matches 365; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1035 CACTTGATAAACAGTGCTGTGCAGTTGAGTTTTAACTAAGTAAACCACCATTCTAGGCT 1094
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Qy      1095 TTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTGGGTCCACATGAATC 1154
          |||
Db       307 TTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTGGGTCCACATGAATC 248

Qy      1155 AGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGGAAAAAATAAGGCAT 1214
          |||
Db       247 AGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGGAAAAAATAAGGCAT 188

Qy      1215 GAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACAAATATTGTCAATGT 1274
          |||
Db       187 GAGAAAGCATTGACATCTTCACTTAAGATCTGAACAAAAGAGAACAAATATTGTCAATGT 128

Qy      1275 TTGGACACTTAGGATCTGAAATCTTGGAAATTTTAAAGACCTCTTTTCTATCAGTGTA 1334
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Db 127 TTGGACACTTAGGATCTGAAATCTTGGAATTTTAAGACCTCTTTTCTATCAGTGATAA 68

Qy 1335 AGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATA 1394
 |||||

Db 67 AGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCATTGGTCAGGTCGATA 8

Qy 1395 AGCGTGT 1401
 |||||

Db 7 AGCGTGT 1

RESULT 13

BB645274

LOCUS BB645274 636 bp mRNA linear EST 31-AUG-2001

DEFINITION BB645274 RIKEN full-length enriched, 4 days neonate male adipose
 Mus musculus cDNA clone B430012021 5', mRNA sequence.

ACCESSION BB645274

VERSION BB645274.1 GI:15402306

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 636)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 prepare full-length cDNA libraries for rapid discovery of new
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 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.

Func. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

1. .636

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="B430012021"

/sex="male"

/tissue_type="adipose"

/dev_stage="4 days neonate"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 4 days neonate male adipose"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 229.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 170 a 118 c 140 g 207 t 1 others
ORIGIN

Query Match 23.2%; Score 357.6; DB 10; Length 636;
Best Local Similarity 91.7%; Pred. No. 1.8e-63;
Matches 389; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

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Qy      1 GCTCCTGGCAGAGTTTTCTGTCTGAGACAGAAGCCGACAGCAGAATGGCACAGAATTTATC 60
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Db      20 GCTCCTGGCAGAGTTTTCTGTCTGAGACAGAAGCCGACAGCAGAATGGCACAGAATTTATC 79

Qy     61 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTTA 120
          |||
Db     80 TTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGGATTTTA 139

Qy    121 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCTT 180
          |||
Db    140 TGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGGGGTGTTCGGGTACCTGTT 199
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 Db 260 TGCTTTCCTGGGCACCCTTCCCATCCTGATAAAGAGTTTGGCCAATGATAAGGGGACCTA 319
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 Qy 420 AACA 423
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 Db 440 AAAA 443

RESULT 14

BB846608

LOCUS BB846608 416 bp mRNA linear EST 26-NOV-2001

DEFINITION BB846608 RIKEN full-length enriched, adult male kidney *Mus musculus* cDNA clone F530003I24 5', mRNA sequence.

ACCESSION BB846608

VERSION BB846608.1 GI:17084983

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 416)

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

JOURNAL Unpublished

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 URL: http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

1. .416

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="F530003I24"

/sex="male"

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="SOLR"

/clone_lib="RIKEN full-length enriched, adult male kidney"

/note="Site_1: XhoI; Site_2: SstI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTTTT 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. Second strand cDNA was prepared with the

primer adapter of sequence [5'

GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTAATTAACCCCCCCCCC 3'].

cDNA was cleaved with XhoI and SstI. "

BASE COUNT 107 a 93 c 87 g 129 t

ORIGIN

Query Match 23.0%; Score 354.2; DB 10; Length 416;

Best Local Similarity 97.3%; Pred. No. 8.7e-63;

Matches 392; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

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RESULT 15

BY368584

LOCUS BY368584 408 bp mRNA linear EST 12-DEC-2002

DEFINITION BY368584 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430110C01 3', mRNA sequence.

ACCESSION BY368584

VERSION BY368584.1 GI:26598072

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 408)

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Cojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, P.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.

, Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES Location/Qualifiers

source 1. .408
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/mol_type="mRNA"
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/clone="F430110C01"
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BASE COUNT 145 a 58 c 63 g 141 t 1 others

ORIGIN

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Best Local Similarity 98.0%; Pred. No. 4.8e-62;
Matches 386; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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Job time : 3525 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 10:09:19 ; Search time 450 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	592.4	38.4	1436	24	ABL90790	Human polynucleoti
6	592.4	38.4	1473	25	ACC46165	Human dithp recept
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22	126.6	8.2	1179	25	AAD50883	Human TARZAN cDNA
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24	126.6	8.2	1729	22	AAS08362	Human cDNA encodin
25	126.6	8.2	1729	23	ABV24026	Human prostate exp
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36	125	8.1	1851	24	ABS51678	DNA encoding human
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c 40	112.6	7.3	740	23	ABV15662	Human prostate exp
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ALIGNMENTS

RESULT 1

ABK12957

ID ABK12957 standard; DNA; 1543 BP.

XX

AC ABK12957;

XX

DT 09-APR-2002 (first entry)

XX

DE DNA sequence of mouse G-protein coupled receptor TGR18 gene.

XX

KW Mouse; G-protein coupled; receptor; GPCR; TGR18; kidney disease;
KW signal transduction modulator; cerebral cavernous malformation;
KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;
KW spleen-associated disorder; immune disorder; gene; ds.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 44..997

FT /*tag= a

FT /product= "Mouse G-protein coupled receptor TGR18"

XX

PN WO200200719-A2.

XX

PD 03-JAN-2002.

XX

PF 25-JUN-2001; 2001WO-US20363.

XX

PR 23-JUN-2000; 2000US-213461P.

XX

PA (TULA-) TULARIK INC.

XX

PI Lin DC, Zhao J, Chen J, Cutler G;

XX

DR WPI; 2002-147880/19.

DR P-PSDB; AAU74904.

XX

PT New G-protein coupled receptor polypeptides, useful for identifying
PT modulators of signal transduction for treating kidney disease,
PT hyperlipidemia, obesity, dyslexia and cardiac myxoma -

XX

PS Claim 18; Page 58; 78pp; English.

XX

CC The present invention relates to a new G-protein coupled receptor (GPCR)
CC polypeptide comprising greater than 70% amino acid sequence identity to
CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18
CC or 90% amino acid sequence identity to human novel edg receptor protein,
CC as defined in the specification. The GPCR covalently linked to a solid
CC phase is useful for identifying a compound that modulates signal
CC transduction. The identified compounds are useful for treating
CC kidney disease, cerebral cavernous malformations, hyperlipidemia,
CC obesity, dyslexia and cardiac myxoma. The molecules of the invention are
CC useful for diagnosing disorders or conditions such as kidney-related
CC conditions or diseases such as renal failure, nephritis, nephrotic

CC syndrome, asymptomatic urinary abnormalities, renal tubule defects,
CC hypertension and nephrolithiasis, liver-related disease or condition
CC e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice
CC and spleen-associated disorders or conditions e.g. splenic enlargement,
CC immune disorders, blood disorders and others. Modulation of the
CC polypeptide of the invention is useful to treat or prevent any of the
CC above conditions or diseases. The present nucleic acid sequence encodes
CC the mouse GPCR TGR18 protein of the invention. This sequence encodes one
CC of seven novel G protein coupled receptors of the invention (ABK12957-
CC ABK12964).

XX

SQ Sequence 1543 BP; 438 A; 352 C; 293 G; 460 T; 0 other;

Query Match 100.0%; Score 1543; DB 24; Length 1543;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
Db 421 ACACCTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCTTAGT 480

Qy 481 GACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGGGCAG 540
|
Db 481 GACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGGGCAG 540

Qy 541 TAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTG 600
|
Db 541 TAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCCTCTG 600

Qy	601	CCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGAT	660
Db	601	CCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACAAGAT	660
Qy	661	GGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACC	720
Db	661	GGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACAAACC	720
Qy	721	CCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATAT	780
Db	721	CCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATCATAT	780
Qy	781	CATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAA	840
Db	781	CATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCACAAGGATGTACACAGAA	840
Qy	841	GGCCATCAAATCTATATACACACTGACACGGCCTCTGGCCTTCTGAACAGTGCCATCAA	900
Db	841	GGCCATCAAATCTATATACACACTGACACGGCCTCTGGCCTTCTGAACAGTGCCATCAA	900
Qy	901	TCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAG	960
Db	901	TCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAGATGCTGATTAGTAAGTTCAG	960
Qy	961	ACAATACTTCAAGTCCCTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACT	1020
Db	961	ACAATACTTCAAGTCCCTTACATCCTTCAGGACATGAGCTGCTGGATGCAGGTCTTCACT	1020
Qy	1021	CAGCCAAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTTAACTAAGTAAACC	1080
Db	1021	CAGCCAAAATGAGACACTTGATAAACAGTGCTGTGCAGTTGAGTTTTAACTAAGTAAACC	1080
Qy	1081	ACCATTTCTAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTG	1140
Db	1081	ACCATTTCTAGGCTTTAGCTTTCCACCATCCTCCAACCCCCAGGGCTGGAGTACAAGCTG	1140
Qy	1141	GGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGG	1200
Db	1141	GGTCCACATGAATCAGAAGGCAGCTCTCTGTTCTGATTTTAGGTTATACCCAGAGTATGG	1200
Qy	1201	AAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACA	1260
Db	1201	AAAAAATAAGGCATGAGAAAGCATTGACATCTTCACTTAAGAACTGAACAAAAGAGAACA	1260
Qy	1261	AATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTT	1320
Db	1261	AATATTGTCAATGTTTGGACACTTAGGATCTGAAATCTTGAAATTTTAAGACCTCTTTT	1320
Qy	1321	TCTATCAGTGTAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCAT	1380
Db	1321	TCTATCAGTGTAAGGAATACAAGATAGCTAGTTGCAAATGCTGAATGCATTTTCATCAT	1380
Qy	1381	TGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTATTTTATTCTTGTAATATTAAAA	1440
Db	1381	TGGTCAGGTCGATAAGCGTGTTTCTGAAATAGTCTTATTTTATTCTTGTAATATTAAAA	1440
Qy	1441	TTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTTCTATTTGAAAATTAT	1500

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Db      1441 TTTATGTGAAAAATGAATATAATTCAATGTACAACATTAGATTTTCTATTTGAAAATTAT 1500
Qy      1501 ATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543
Db      1501 ATTTCTTGAAAAAATAACTGCTGTGCCTAAATAAATCAATATA 1543

```

RESULT 2

AAD01135

ID AAD01135 standard; cDNA; 1005 BP.

XX

AC AAD01135;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human orphan G protein-coupled receptor hCHN10 cDNA.

XX

KW Human; orphan G protein-coupled receptor; GPCR; hCHN10; drug screening;

KW transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1005

FT /*tag= a

FT /product= "hCHN10"

FT /note= "Human orphan G protein-coupled receptor"

XX

PN WO200031258-A2.

XX

PD 02-JUN-2000.

XX

PF 13-OCT-1999; 99WO-US23687.

XX

PR 20-NOV-1998; 98US-0109213.

PR 16-FEB-1999; 99US-0120416.

PR 26-FEB-1999; 99US-0121852.

PR 12-MAR-1999; 99US-0123946.

PR 12-MAR-1999; 99US-0123949.

PR 28-MAY-1999; 99US-0136436.

PR 28-MAY-1999; 99US-0136437.

PR 28-MAY-1999; 99US-0136439.

PR 28-MAY-1999; 99US-0136567.

PR 28-MAY-1999; 99US-0137127.

PR 28-MAY-1999; 99US-0137131.

PR 29-JUN-1999; 99US-0141448.

PR 29-SEP-1999; 99US-0156555.

PR 29-SEP-1999; 99US-0156633.

PR 29-SEP-1999; 99US-0156634.

PR 29-SEP-1999; 99US-0156653.

PR 01-OCT-1999; 99US-0157280.

PR 01-OCT-1999; 99US-0157281.

PR 01-OCT-1999; 99US-0157282.

PR 01-OCT-1999; 99US-0157293.

PR 01-OCT-1999; 99US-0157294.

PR 12-OCT-1999; 99US-0416760.

KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical;
 KW mutant; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US24065.
 XX
 PR 13-OCT-1998; 98US-0170496.
 PR 12-NOV-1998; 98US-0108029.
 PR 20-NOV-1998; 98US-0109213.
 PR 27-NOV-1998; 98US-0110060.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123944.
 PR 12-MAR-1999; 99US-0123945.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123948.
 PR 12-MAR-1999; 99US-0123949.
 PR 12-MAR-1999; 99US-0123951.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 28-MAY-1999; 99US-0137567.
 PR 30-JUN-1999; 99US-0141448.
 PR 27-AUG-1999; 99US-0151114.
 PR 03-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156634.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX
 DR WPI; 2000-317986/27.
 DR P-PSDB; AAB02842.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents -
 XX
 PS Example 1; Page 116; 187pp; English.
 XX
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.

CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.

XX

SQ Sequence 1005 BP; 248 A; 236 C; 196 G; 325 T; 0 other;

Query Match 38.4%; Score 592.4; DB 21; Length 1005;
Best Local Similarity 75.5%; Pred. No. 3.2e-140;
Matches 750; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

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Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      8 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 67

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     68 AGTACTACCTTTCCATTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 127

Qy     159 CTGTGGTGTTCGGCTACCTCTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     128 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 187

Qy     219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     188 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCATGCTGATAAGGAGTT 247

Qy     279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     248 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 307

Qy     339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     308 ATGCCAACCTCTATACCAGCATCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA 367

Qy     399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     368 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 427

Qy     459 CGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     428 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 487

Qy     519 CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     488 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 547

Qy     579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     548 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 607

Qy     639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGCCAGCAGCAAGCAA 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     608 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 667

Qy     699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA 758
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     668 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 727
```


DR WPI; 2003-046718/04.

DR P-PSDB; ABP81696.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

XX

SQ Sequence 1380 BP; 383 A; 294 C; 274 G; 429 T; 0 other;

Query Match 38.4%; Score 592.4; DB 25; Length 1380;
Best Local Similarity 75.3%; Pred. No. 3.7e-140;
Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

Qy	39	GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA	98
Db	50	GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA	109
Qy	99	AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA	158
Db	110	AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAATACCA	169
Qy	159	CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT	218
Db	170	TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT	229
Qy	219	TTAACCTTTCCATCTCTGACTTTGCTTTTCTGTGCACCCTTCCCATCTGATAAAGAGTT	278
Db	230	TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCTGCTGATAAGGAGTT	289

XX
 AC ABL90790;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 1352.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16450.
 XX
 PR 19-MAY-2000; 2000US-205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-122018/16.
 DR P-PSDB; ABB90381.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -
 XX
 PS Claim 4; SEQ ID NO 1352; 2081pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1436 BP; 397 A; 309 C; 289 G; 441 T; 0 other;

Query Match 38.4%; Score 592.4; DB 24; Length 1436;
Best Local Similarity 75.3%; Pred. No. 3.7e-140;
Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

```
Qy      39 GCAGAATGGCACAGAATTTATCTTGAGAAATGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     100 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 159

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     160 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 219

Qy     159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     220 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 279

Qy     219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     280 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCATGCTGATAAGGAGTT 339

Qy     279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     340 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 399

Qy     339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     400 ATGCCAACCTCTATACCAGCATCTCTTTCTCACTTTATCAGCATAGATCGATACTTGA 459

Qy     399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     460 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 519

Qy     459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     520 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 579

Qy     519 CTGTCCCAAAAGAAGAGGGCAGTAACCTGCATCGACTATGCAAGTTCTGGAACCCCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     580 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 639

Qy     579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     640 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 699

Qy     639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     700 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 759

Qy     699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA 758
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     760 CTGCTCTGCCCCTTGAAAGCCTCTCAACTTGGTCATCATGGCAGTGGAATCTTCTCTG 819

Qy     759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     820 TGCTTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 879
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Qy	819	G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC	875
Db	880	GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT	939
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA	935
Db	940	TGGCCTTTCTGAACAGTGTCAACCTGCTTCTATTTTCTTTTGGGAGATCACTTCA	999
Qy	936	GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT	995
Db	1000	GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT	1059
Qy	996	GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG	1048
Db	1060	GGGCTCATGAACTCCTACTTTTCATTCAGAGAAAAAGTGAGGGGCTTGTGAAACAG	1113

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-129518/12.

DR P-PSDB; ABR41222.

XX

PT Novel human diagnostic and therapeutic polypeptide useful for
PT identifying test compound which specifically binds to a polypeptide
PT encoded by human diagnostic and therapeutic polynucleotide, and to
PT induce antibodies -

XX

PS Claim 2; SEQ ID No 86; 591pp; English.

XX

CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
CC to polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods
CC of detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dithp cDNA encoding a DITHP protein
CC which has receptor activity.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1473 BP; 403 A; 320 C; 303 G; 447 T; 0 other;

Query Match 38.4%; Score 592.4; DB 25; Length 1473;
Best Local Similarity 75.3%; Pred. No. 3.8e-140;
Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

Qy 39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
| | ||||| ||| | ||| | || |||| ||||| | || |
Db 119 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 178

Qy 99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158

Db 179 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGAAATACCA 238
 Qy 159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
 Db 239 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 298
 Qy 219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
 Db 299 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCATGCTGATAAGGAGTT 358
 Qy 279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
 Db 359 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 418
 Qy 339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
 Db 419 ATGCCAACCTCTATACCAGCATCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA 478
 Qy 399 TCATGAAGTACCCTTTCCGAGAACACCTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
 Db 479 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 538
 Qy 459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
 Db 539 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 598
 Qy 519 CTGTCCCAAGAAGAGGGCAGTAACCTGCATCGACTATGCAAGTTCTGGAAACCCTGAAC 578
 Db 599 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGAAGTTCTGGAGACCCCAACT 658
 Qy 579 ACAATCTCATTTACAGCCTCTGCC'TGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
 Db 659 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA 718
 Qy 639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
 Db 719 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 778
 Qy 699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA 758
 Db 779 CTGCTCTGCCCTTGAAAAGCCTCTCAACTTGGTCAATCATGGCAGTGGTAATCTTCTCTG 838
 Qy 759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
 Db 839 TGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 898
 Qy 819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
 Db 899 GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT 958
 Qy 876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCTCATGGGAGACCATTACA 935
 Db 959 TGGCCTTTCTGAACAGTGTCAATCAACCCTGTCTTCTATTTTCTTTTGGGAGATCACTTCA 1018
 Qy 936 GAGAGATGCTGATTAGTAAGTTTCAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995

Db 1019 GGGACATGCTGATGAATCAACTGAGACACAACCTTCAAATCCCTTACATCCTTTAGCAGAT 1078

Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
 | | | | | | | | | | | | | | | | | | | | | |

Db 1079 GGGCTCATGAACTCCTACTTTTCATTGAGAGAAAAGTGAGGGGCTTGTGAAACAG 1132

RESULT 7

AAD24958

ID AAD24958 standard; cDNA; 1542 BP.

XX

AC AAD24958;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human G-protein coupled receptor-3 (GCREC-3) cDNA.

XX

KW Human; G-protein coupled receptor-3; GCREC-3; therapy; cancer; stroke;
 KW cell proliferative disorder; neurological; epilepsy; Parkinson's disease;
 KW Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS;
 KW Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis;
 KW multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis;
 KW diabetes; ulcer; viral infection; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 63..1202

FT /*tag= a

FT /product= "Human GCREC-3 protein"

XX

PN WO200198351-A2.

XX

PD 27-DEC-2001.

XX

PF 15-JUN-2001; 2001WO-US19275.

XX

PR 16-JUN-2000; 2000US-212483P.

PR 22-JUN-2000; 2000US-213954P.

PR 29-JUN-2000; 2000US-215209P.

PR 07-JUL-2000; 2000US-216595P.

PR 14-JUL-2000; 2000US-218936P.

PR 19-JUL-2000; 2000US-219154P.

PR 21-JUL-2000; 2000US-220141P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lal P, Baughn MR, Hafalia AJA, Nguyen DB, Gandhi AR, Kallick DA;
 PI Griffin JA, Yue H, Khan FA, Patterson C, Lu DAM, Tribouley CM;
 PI Lu Y, Walia NK, Graul R, Yao MG, Yang J, Ramkumar J, Au-Young J;
 PI Elliott VS, Hernandez R, Walsh RT, Borowsky ML, Thornton M, He A;

XX

DR WPI; 2002-075627/10.

DR P-PSDB; AAE15633.

XX

PT Isolated human G-protein coupled receptor polypeptides and the use of
 PT these sequences in the diagnosis, treatment and prevention of diseases

PT and in the assessment of exogenous compounds on the expression of the
PT receptors -

XX

PS Claim 11; Page 133; 143pp; English.

XX

CC The invention relates to isolated human G-protein coupled receptor
CC (GCREC) polypeptides and their biologically active fragments. GCREC and
CC protein is useful in treating a disease or condition associated with an
CC increase or decrease in expression of functional GCREC. The GCREC's are
CC useful in the diagnosis, treatment and prevention of cell proliferative
CC disorders (cancer, leukaemia, melanoma); neurological disorders (stroke,
CC epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune
CC inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
CC sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris),
CC gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis),
CC metabolic disorders (diabetes); viral infections (herpes virus) and in
CC the assessment of the effects of exogenous compounds on the expression
CC of the nucleic acid and amino acid sequences. The present sequence is
CC human GCREC-3 cDNA.

XX

SQ Sequence 1542 BP; 428 A; 327 C; 315 G; 472 T; 0 other;

Query Match 38.4%; Score 592.4; DB 24; Length 1542;
Best Local Similarity 75.3%; Pred. No. 3.8e-140;
Matches 764; Conservative 0; Mismatches 246; Indels 4; Gaps 2;

Qy 39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 264

Qy 99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA 158
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 265 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 324

Qy 159 CTGTGGTGTTCGGCTACCTCTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 325 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 384

Qy 219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 385 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 444

Qy 279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 445 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 504

Qy 339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC 398
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 505 ATGCCAACCTCTATACCAGCATTCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA 564

Qy 399 TCATGAAGTACCCTTTCCGAGAACACTTCTACAAAAGAAGGAATTGCCATTTTAATCT 458
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 565 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 624

Qy 459 CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 625 CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 684

Qy	519	CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCCTGAAC	578
Db	685	CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGAAGTTCTGGAGACCCCAACT	744
Qy	579	ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA	638
Db	745	ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA	804
Qy	639	TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA	698
Db	805	TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA	864
Qy	699	CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA	758
Db	865	CTGCTCTGCCCTTGAAAAGCCTCTCAACTGGTCATCATGGCAGTGGTAATCTTCTCTG	924
Qy	759	TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT	818
Db	925	TGCTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT	984
Qy	819	G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC	875
Db	985	GGAAGCAGTATCAGTGCCTCAGGTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT	1044
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA	935
Db	1045	TGGCCTTTCTGAACAGTGTCAACCCCTGTCTTCTATTTTCTTTTGGGAGATCACTTCA	1104
Qy	936	GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT	995
Db	1105	GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT	1164
Qy	996	GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG	1048
Db	1165	GGGCTCATGAACCTCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTTGTGAAACAG	1218

RESULT 8

ABS57291

ID ABS57291 standard; cDNA; 1338 BP.

XX

AC ABS57291;

XX

DT 30-JAN-2003 (first entry)

XX

DE cDNA encoding human adenosine receptor.

XX

KW Human; mammalian; adenosine receptor; G-protein coupled receptor;
 KW GPCR; adenosine-mediated medical condition; vasodilation; hypotension;
 KW reversal of tachycardia; chronic renal disease; thyroid disorder;
 KW inflammation; asthma; hypertensive; antiarrhythmic; antiinflammatory;
 KW antiasthmatic; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

```

FT      CDS          1..1005
FT      /*tag= a
FT      /product= "Adenosine receptor"
XX
PN      US2002137887-A1.
XX
PD      26-SEP-2002.
XX
PF      17-JAN-2001; 2001US-0765034.
XX
PR      17-JAN-2001; 2001US-0765034.
XX
PA      (HEDR/) HEDRICK J A.
PA      (LACH/) LACHOWICZ J E.
PA      (WANG/) WANG W.
PA      (GUST/) GUSTAFSON E L.
XX
PI      Hedrick JA, Lachowicz JE, Wang W, Gustafson EL;
XX
DR      WPI; 2003-074992/07.
DR      P-PSDB; ABG72131.
XX
PT      Novel isolated mammalian adenosine receptor polypeptide useful for
PT      identifying an agonist or antagonist of the receptor for treating
PT      vasodilation, hypotension, chronic renal diseases, thyroid disorders
PT      and inflammation -
XX
PS      Example 1; Page 14-16; 19pp; English.
XX
CC      The present invention relates to the isolation of a mammalian
CC      (human) adenosine receptor, and the polynucleotide sequence
CC      encoding it. The cloned receptor resembles a member of the
CC      G-protein coupled receptor (GPCR) superfamily that contains
CC      7-transmembrane domains. The adenosine receptor is useful for
CC      identifying agonists and antagonists of the receptor, which may be
CC      useful for treating an adenosine-mediated medical condition. The
CC      adenosine receptor polypeptide sequence is also useful as an
CC      antigen to elicit antibody production in an immunologically
CC      competent host. An antibody which binds specifically to the
CC      adenosine receptor is useful for treating medical conditions caused
CC      or mediated by adenosine such as vasodilation, hypotension, reversal
CC      of tachycardia, chronic renal diseases, thyroid disorders and
CC      inflammation (e.g. asthma). The antibody can also be used to purify
CC      the adenosine receptor, or as a basis for immunoassays of the receptor.
CC      The polynucleotide sequence encoding the adenosine receptor is useful
CC      for producing vectors and host cells containing the vectors. It is
CC      also useful for measuring expression of a mammalian adenosine
CC      receptor gene in a biological sample. The present sequence encodes
CC      human adenosine receptor.
XX
SQ      Sequence 1338 BP; 370 A; 288 C; 265 G; 415 T; 0 other;

Query Match          38.3%; Score 590.8; DB 25; Length 1338;
Best Local Similarity 75.2%; Pred. No. 9.2e-140;
Matches 763; Conservative 0; Mismatches 247; Indels 4; Gaps 2;

Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98

```

Db	8	GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA	67
Qy	99	AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA	158
Db	68	AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGAAATACCA	127
Qy	159	CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT	218
Db	128	TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT	187
Qy	219	TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT	278
Db	188	TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT	247
Qy	279	ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC	338
Db	248	ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC	307
Qy	339	ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGC	398
Db	308	ATGCCAACCTCTATACCAGCATCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA	367
Qy	399	TCATGAAGTACCCTTTCCGAGAACACTTCTACAAAAGAAGGAATTTGCCATTTTAATCT	458
Db	368	TAATTAAGTATCCTTTCCGAGAACACTTCTGCAAAGAAAGAGTTTGCTATTTTAATCT	427
Qy	459	CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT	518
Db	428	CCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC	487
Qy	519	CTGTCCCAAAGAAGAGGGCAGTAAC'TGCATCGACTATGCAAGTTCTGGAAACCCCTGAAC	578
Db	488	CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT	547
Qy	579	ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA	638
Db	548	ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTGTGA	607
Qy	639	TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA	698
Db	608	TGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAGGTTGCTA	667
Qy	699	CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA	758
Db	668	CTGCTCTGCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG	727
Qy	759	TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT	818
Db	728	TGCCTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT	787
Qy	819	G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC	875
Db	788	GGAAGCAGTATCAGTGAAGTCAAGTTCGTCATCAACTCCTTTTACATTGTGACACGGCCTT	847
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA	935


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FT          /*tag= e
FT          /note= "binding site for primer used to amplify
FT              cDNA for bacterial expression"
FT primer_bind 1085..1096
FT          /*tag= f
FT          /note= "binding site for primer used to amplify
FT              cDNA for baculovirus expression"
XX
PN WO9724929-A1.
XX
PD 17-JUL-1997.
XX
PF 11-JAN-1996; 96WO-US00392.
XX
PR 11-JAN-1996; 96WO-US00392.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y;
XX
DR WPI; 1997-372505/34.
DR P-PSDB; AAW22732.
XX
PT Isolated human ATP receptor - agonists and antagonists of which are
PT useful in treatment of, e.g. asthma, hypertension, arterial
PT thrombosis and psychotic and neurological disorders
XX
PS Claim 7; Fig 1A-C; 53pp; English.
XX
CC A cDNA clone (AAT75146) codes for human ATP receptor (AAW22732), a
CC polypeptide structurally related to the G protein-coupled receptor
CC family. It was discovered in a human placenta cDNA library.
CC cDNA encoding the mature receptor, deposited as ATCC 97333, can
CC be expressed in bacterial (e.g. E. coli), mammalian (e.g. COS) or
CC insect (e.g. Sf9) host cells and used to screen for agonists and
CC antagonists useful in the treatment of a variety of disorders.
CC It can also be used to identify a mutation in an ATP receptor gene
CC and thus to diagnose diseases, or susceptibility to diseases,
CC related to ATP receptor underexpression.
XX
SQ Sequence 1428 BP; 394 A; 308 C; 290 G; 435 T; 1 other;

Query Match          38.1%; Score 587.2; DB 18; Length 1428;
Best Local Similarity 75.0%; Pred. No. 7.8e-139;
Matches 760; Conservative 1; Mismatches 249; Indels 4; Gaps 2;

Qy          39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          99 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 158

Qy          99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCA 158
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        159 AGTACTACCTTTCCATTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 218

Qy        159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        219 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 278

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Qy	219	TTAACCTTTCCATCTCTGACTTTGCTTTCCCTGTGCACCCTTCCCATCCTTGATAAAAGAGTT	278
Db	279	TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT	338
Qy	279	ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC	338
Db	339	ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC	398
Qy	339	ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGC	398
Db	399	ATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGATACTTGA	458
Qy	399	TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT	458
Db	459	TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTGTGCTATTTTAATCT	518
Qy	459	CGCTGGCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT	518
Db	519	CCTTGGCCATGTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCTTATAAATC	578
Qy	519	CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAAC	578
Db	579	CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT	638
Qy	579	ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA	638
Db	639	ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCTTATTCTCTTTTGTGA	698
Qy	639	TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA	698
Db	699	TGTGTTTCTTTTATTACAAGATTGCCTCCTTCCTAAAGCAGAGGAATAGGCAGGTTGCTA	758
Qy	699	CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTA	758
Db	759	CTGCCTCGCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG	818
Qy	759	TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT	818
		:	
Db	819	TGCTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTGGGAGTT	878
Qy	819	G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC	875
Db	879	GGAAGCAGTATCAGTGCCTCAGGTCGTCACTCAACTCCTTTTACATTGTGACACGGCCTG	938
Qy	876	TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACA	935
Db	939	TGGCCTTTCTGAACAGTGTCAATCAACCCTGTCTTCTATTTTCTGTGGGAGATCACTTCA	998
Qy	936	GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT	995
Db	999	GGGACATGCTGATGAATCAACTGAGACACAACCTTCAAATCCCTTACATCCTTTAGCAGAT	1058
Qy	996	GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAA-TGAGACACTTGATAAACAG	1048
Db	1059	GGGCTCATGAACTCCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTTGTGAAACAG	1112

RESULT 11

AAC81122

ID AAC81122 standard; cDNA; 1385 BP.

XX

AC AAC81122;

XX

DT 14-FEB-2001 (first entry)

XX

DE Human secreted protein gene 37 SEQ ID NO:47.

XX

KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW cerebrovascular disorder; nervous system disorder; infection; skin aging;
KW ocular disorder; wound healing; food additive; preservative; ss.

XX

OS Homo sapiens.

XX

PN WO200061628-A1.

XX

PD 19-OCT-2000.

XX

PF 06-APR-2000; 2000WO-US09070.

XX

PR 09-APR-1999; 99US-0128695.

PR 14-JAN-2000; 2000US-0176052.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM, Komatsoulis G;

XX

DR WPI; 2000-619228/59.

DR P-PSDB; AAB45344.

XX

PT New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -

XX

PS Claim 1; Page 412; 454pp; English.

XX

CC The polynucleotide sequences given in AAC81086 to AAC81134 encode the
CC human secreted proteins given in AAB45308 to AAB45356. AAB45357 to
CC AAB45384 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
CC and vulnerary. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include

CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC disorders, cerebrovascular disorders, angiogenesis, nervous system
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC disorders. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. AAC81077 to AAC81085 and AAB45307 represent sequences used in
CC the exemplification of the present invention.

XX

SQ Sequence 1385 BP; 385 A; 296 C; 275 G; 429 T; 0 other;

Query Match 37.6%; Score 580.4; DB 21; Length 1385;
Best Local Similarity 75.2%; Pred. No. 4.1e-137;
Matches 763; Conservative 0; Mismatches 246; Indels 5; Gaps 3;

```
Qy      39 GCAGAATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATA 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      56 GGATCATGGCATGGAATGCAACTTGCAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAA 115

Qy      99 AGTACTACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCA 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     116 AGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCA 175

Qy     159 CTGTGGTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTT 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     176 TTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATTTATCTCT 235

Qy     219 TTAACCTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTT 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     236 TTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTT 295

Qy     279 ATGCCAATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTC 338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     296 ATGCCAATGGAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTC 355

Qy     339 ACACCAACCTCTACACCAGCATCCTCTTCCTCACTTTTCATTAGCATGGACCGATATCTGC 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     356 ATGCCAACCTCTATACCAGCATCTCTTCTCACTTTTATCAGCATAGATCGATACTTGA 415

Qy     399 TCATGAAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCT 458
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     416 TAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCT 475

Qy     459 CGCTGGCTGTCTGGGCCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATT 518
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     476 CTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTTATAAATC 535

Qy     519 CTGTCCCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAAC 578
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     536 CTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACT 595

Qy     579 ACAATCTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGA 638
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Db 596 ACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCTCTTTTTGTGA 655

Qy 639 TGTGCTTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAA 698
 |||| |||| | ||||| | |||| |||| |||| |||| |||

Db 656 TGTGTTTCTTTTATTACAAGATTGCTCTCTTCTTAAAGCAGAGGAATAGGCAGGTTGCTA 715

Qy 699 CTGCCCTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTA 758
 |||| |||| | || || || | |||| || |||| || || |||||

Db 716 CTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTG 775

Qy 759 TACTCTTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTT 818
 | || || ||||| ||||| || ||||| ||||| ||||| ||||

Db 776 TGCTTTTACACCCTATCACGTGATGCGGAATGTGAGGATCGCTTCACGCCTGGGGAGTT 835

Qy 819 G---GCCACAAGGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTC 875
 | || | || || || | |||| || | |||| ||||| ||||

Db 836 GGAAGCAGTATCAGTGCCTCAGGTCGTCACTCAACTCCTTTTACATTGTGACAC-GCCTT 894

Qy 876 TGGCCTTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCCTCATGGGAGACCATTACA 935
 ||||| ||||| ||||| || ||||| || || ||||| || || ||

Db 895 TGGCCTTTCTGAACAGTGCATCAACCCTGTCTTCTATTTTCTTTTGGGAGATCACTTCA 954

Qy 936 GAGAGATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTCAGGACAT 995
 | || ||||| || | | |||| ||||| ||||| ||||| || || ||

Db 955 GGGACATGCTGATGAATCAACTGAGACACAACCTCAAATCCCTTACATCCTTTAGCAGAT 1014

Qy 996 GAGCTGCTGGATGCAGGTCTTCACTCAGCCAAAA-TGAGACACTTGATAAACAG 1048
 | ||| || | | |||| |||| |||| |||| |||| |||||

Db 1015 GGGCTCATGAACTCCTACTTTTCATTTCAGAGAAAAGTGAGGGGCTTGTGAAACAG 1068

RESULT 12

AAL43942

ID AAL43942 standard; DNA; 1011 BP.

XX

AC AAL43942;

XX

DT 27-SEP-2002 (first entry)

XX

DE Human G protein-coupled receptor coding sequence.

XX

KW Human; gene therapy; G protein-coupled receptor; drug development;
 KW central nervous system disease; endocrine disease; metabolic disease;
 KW cancer; respiratory disease; digestive disease; immune disease;
 KW inflammation; infection; circulatory disease; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1011

FT /*tag= a

FT /partial

FT /product= "Human G-protein coupled receptor"

FT /note= "No stop codon is given"

XX

PN WO200257441-A1.

XX

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FD      25-JUL-2002.
XX
PF      17-JAN-2002; 2002WO-JP00270.
XX
PR      18-JAN-2001; 2001JP-0010714.
PR      30-MAR-2001; 2001JP-0102484.
XX
PA      (TAKE ) TAKEDA CHEM IND LTD.
XX
PI      Miwa M, Ito T, Shintani Y, Miyajima N;
XX
DR      WPI; 2002-566800/60.
DR      P-PSDB; AAO15399.
XX
PT      Human kidney-originated G protein-coupled receptor protein TGR30 and
PT      encoded DNA, for developing drugs to treat central nervous diseases,
PT      endocrine diseases, metabolic diseases and cancer, including gene
PT      therapy -
XX
PS      Claim 6; Page 90-91; 98pp; Japanese.
XX
CC      The invention comprises the amino acid and coding sequence of a human G
CC      protein-coupled receptor. The DNA and protein sequences of the invention
CC      are useful for developing drugs to prevent or treat (gene therapy):
CC      central nervous system diseases; endocrine diseases; metabolic diseases;
CC      cancer; respiratory diseases; digestive diseases; immune diseases;
CC      inflammations; infections; and circulatory diseases. The present DNA
CC      sequence encodes the human G protein-coupled receptor of the invention.
XX
SQ      Sequence 1011 BP; 257 A; 263 C; 188 G; 303 T; 0 other;

Query Match          8.2%; Score 126.6; DB 24; Length 1011;
Best Local Similarity 49.9%; Pred. No. 6.2e-22;
Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      ||| || ||||| | | | | ||| ||| ||| |||
Db      59 CTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 118

Qy      120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCAGTGTGGTGTTCGGCTACCTCT 179
      ||| || ||| | | ||| | | ||| ||| ||| |||
Db      119 ATGGCATTATCTTCCTCGTGGGATTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178

Qy      180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTTAACCTTTCCATCTCTGACT 239
      || |||| |||| ||||| || | | | |||| || | | |
Db      179 TCAAATGAGACCTTGGAAGAGCAGCACCATCATATGCTGAACCTGGCCTGCACAGATC 238

Qy      240 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
      | | | ||| ||| ||| ||||| | ||||| | ||| |||
Db      239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298

Qy      297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
      || ||||| | | ||| | ||| | || ||||| ||| ||
Db      299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 358

Qy      357 GCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
      ||||| ||||| ||| | |||| | ||| | ||| | ||| |

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Db 359 GCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCAATGA 418

Qy 417 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCT 476
| | | | | | | | | | | | | | | |

Db 419 GCTGCTTTTCCATTACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478

Qy 477 TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCCAAAGAAGAGG 536
| | | | | | | | | | | | | | | |

Db 479 TTTCACTGGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA 538

Qy 537 GCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCC 596
| | | | | | | | | | | | | | | |

Db 539 GATCAGCCTGTCTCGACCTCACCAGTTCGG-----ATGAACCTCAATACTATTAAGTGGT 592

Qy 597 TCTGCCTGACTTTGTGGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA 656
| | | | | | | | | | | | | | | |

Db 593 ACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCT 652

Qy 657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
| | | | | | | | | | | | | | | |

Db 653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACCTGACAGCTGCCTTAAGCAGA 712

Qy 717 AACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
| | | | | | | | | | | | | | | |

Db 713 AAGCACGAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTACCCTTCC 772

Qy 777 ATATCATGCGCAATTTGAGGATCGCCTCACGCCTG 811
| | | | | | | | | | | | | | | |

Db 773 ATATCTTGAGGGTCATTCCGATCGAATCTCGCCTG 807

RESULT 13

AAS07948

ID AAS07948 standard; cDNA; 1014 BP.

XX

AC AAS07948;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human cDNA encoding G-protein coupled receptor, hRUP21.

XX

KW Human; G-protein coupled receptor; GPCR; hRUP21; agonist;

KW inverse agonist; lung cancer; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1014

FT /*tag= a

FT /product= "hRUP21"

XX

PN WO200136471-A2.

XX

PD 25-MAY-2001.

XX

PF 16-NOV-2000; 2000WO-US31509.

XX

PR 17-NOV-1999; 99US-0166088.
PR 17-NOV-1999; 99US-0166099.
PR 17-NOV-1999; 99US-0166369.
PR 23-DEC-1999; 99US-0171900.
PR 23-DEC-1999; 99US-0171901.
PR 23-DEC-1999; 99US-0171902.
PR 11-FEB-2000; 2000US-0181749.
PR 14-MAR-2000; 2000US-0189258.
PR 14-MAR-2000; 2000US-0189259.
PR 10-APR-2000; 2000US-0195898.
PR 10-APR-2000; 2000US-0195899.
PR 10-APR-2000; 2000US-0196078.
PR 28-APR-2000; 2000US-0200419.
PR 12-MAY-2000; 2000US-0203630.
PR 12-JUN-2000; 2000US-0210741.
PR 12-JUN-2000; 2000US-0210982.
PR 21-AUG-2000; 2000US-0226760.
PR 26-SEP-2000; 2000US-0235418.
PR 26-SEP-2000; 2000US-0235779.
PR 20-OCT-2000; 2000US-0242332.
PR 20-OCT-2000; 2000US-0242343.

XX

PA (AREN-) ARENA PHARM INC.

XX

PI Chen R, Dang HT, Lowitz KP;

XX

DR WPI; 2001-355616/37.

DR P-PSDB; AAU04375.

XX

PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -

XX

PS Claim 55; Page 113-114; 159pp; English.

XX

CC The sequence encodes a human G-protein coupled receptor (GPCR),
CC hRUP21 The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer.
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilised to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.

XX

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 8.2%; Score 126.6; DB 22; Length 1014;

Best Local Similarity 49.9%; Pred. No. 6.2e-22;

Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

Qy 60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
||| || ||||| | | | | | | | | | | | |
Db 59 CTTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 118

Qy 120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCT 179

XX
 KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200216548-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-IB01446.
 XX
 PR 04-AUG-2000; 2000JP-0237818.
 PR 13-FEB-2001; 2001JP-0034434.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Haga T, Takeda S, Mitaku S;
 XX
 DR WPI; 2002-304118/34.
 DR P-PSDB; ABP95602.
 XX
 PT Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development -
 XX
 PS Claim 9; SEQ ID NO 13; 97pp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
 CC (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
 CC transmembrane domains with 250-1000 amino acid residues to give a gene
 CC homologous with a known GPCR gene. The receptor proteins and encoded
 CC genes are useful for studying in vivo signal transduction mechanism and
 CC identifying targets for drug development e.g. based on olfactory and
 CC gustatory receptors in form of agonists and antagonists by screening
 CC intrinsic and extrinsic ligands as bitter taste inhibitors, taste
 CC enhancers and fragrance improvers.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 8.2%; Score 126.6; DB 24; Length 1014;
 Best Local Similarity 49.9%; Pred. No. 6.2e-22;
 Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

Qy 60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
 ||| || |||| | | | ||| ||| |||
 Db 59 CTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 118
 Qy 120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACCTGTGGTGTTCGGCTACCTCT 179
 ||| || ||| | | ||| | | || ||| ||| ||| |||
 Db 119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178
 Qy 180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAAACCTTCCATCTCTGACT 239

Db 179 TCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 238
 Qy 240 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
 Db 239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298
 Qy 297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
 Db 299 TCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 358
 Qy 357 GCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
 Db 359 GCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCCAATGA 418
 Qy 417 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCT 476
 Db 419 GCTGCTTTTCCATTCACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478
 Qy 477 TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTTCATCAATTCTGTCCCAAAGAAGAGG 536
 Db 479 TTTCACTGGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA 538
 Qy 537 GCAGTAACCTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAATCTCATTTACAGCC 596
 Db 539 GATCAGCCTGTCTCGACCTCACCAGTTCCG-----ATGAACTCAATACTATTAAGTGGT 592
 Qy 597 TCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA 656
 Db 593 ACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCT 652
 Qy 657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
 Db 653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGA 712
 Qy 717 AACCCCAACGCCTGGTGGTCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
 Db 713 AAGCACGAAGGCTAACCATTCTGCTACTCCTTGCAATTTTACGTATGTTTTTACCCTTCC 772
 Qy 777 ATATCATGCGCAATTTGAGGATCGCCTCACGCCTG 811
 Db 773 ATATCTTGAGGGTCATTCGGATCGAATCTCGCCTG 807

RESULT 15

ABN85630

ID ABN85630 standard; DNA; 1014 BP.

XX

AC ABN85630;

XX

DT 18-SEP-2002 (first entry)

XX

DE Human P2Y-like receptor variant encoding gene SEQ ID NO 3.

XX

KW Human; Py2-like receptor; HIPHUM 0000037; immunity; inflammation;

KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;

KW immunomodulator; anti-inflammatory; cytostatic; antiasthmatic;

KW gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;
 KW antibacterial; immunosuppressive; dermatological; nephrotropic;
 KW antiallergic; analgesic; receptor; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "P2Y-like receptor variant"
 XX
 PN GB2369364-A.
 XX
 PD 29-MAY-2002.
 XX
 PF 31-AUG-2001; 2001GB-0021215.
 XX
 PR 01-SEP-2000; 2000GB-0021524.
 PR 06-SEP-2000; 2000GB-0021894.
 PR 25-SEP-2000; 2000GB-0023444.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Foord SM, Ignar DM;
 XX
 DR WPI; 2002-511268/55.
 DR P-PSDB; ABB83819.
 XX
 PT An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be
 PT used for the identification of agonists and antagonists which may be
 PT used to treat an immune or inflammatory disease -
 XX
 PS Claim 5; Page 28-29; 35pp; English.
 XX
 CC The invention relates to an isolated P2Y-like receptor polypeptide
 CC (ABB83818-ABB83819) which is also referred to in the specification as
 CC HIPHUM 0000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates P2Y receptor activity is useful to treat a
 CC subject having a disorder that is responsive to P2Y-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of P2Y-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polymyositis or prostatitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the P2Y-like receptor variant encoding gene
 CC of the invention.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 8.2%; Score 126.6; DB 24; Length 1014;
 Best Local Similarity 49.9%; Pred. No. 6.2e-22;

Matches 377; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

```

Qy      60 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTACTACCTCTCTGCATTTT 119
      ||| || ||||| | | | | | | | | | | | | | |
Db      59 CTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 118

Qy     120 ATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTGGTGTTCGGCTACCTCT 179
      ||| || ||| | | ||| | | |||| | | | | | | | |
Db     119 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 178

Qy     180 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTTAACCTTTCCATCTCTGACT 239
      || |||| | |||| | |||| | | | | | | | | | |
Db     179 TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 238

Qy     240 TTGCTTTCCTGTGCACCCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 296
      | | | | | | | | | | | | | | | | | | | | | |
Db     239 TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 298

Qy     297 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 356
      || ||||| | | |||| | ||| | | | | | | | | | |
Db     299 TCTTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 358

Qy     357 GCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATGAAGTACCCTTTCC 416
      ||||| | | | | | | | | | | | | | | | | | | |
Db     359 GCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGA 418

Qy     417 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCT 476
      | | | | | | | | | | | | | | | | | | | | | |
Db     419 GCTGCTTTTCCATTACAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 478

Qy     477 TAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTCCCAAAGAAGAGG 536
      | | | | | | | | | | | | | | | | | | | | | |
Db     479 TTTCACTGGTAGCTGTCAATCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACA 538

Qy     537 GCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCTGAACACAATCTCATTTACAGCC 596
      | | | | | | | | | | | | | | | | | | | | | |
Db     539 GATCAGCCTGTCTCGACCTACCAAGTTTCGG-----ATGAACTCAATACTATTAAGTGGT 592

Qy     597 TCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGCTTCTTCTACTACA 656
      | | |||| | | | | | | | | | | | | | | | | | |
Db     593 ACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCT 652

Qy     657 AGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCCCTGCCACTGGACA 716
      | | | | | | | | | | | | | | | | | | | | | |
Db     653 ATACCACGATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGA 712

Qy     717 AACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTCTTCACACCCTATC 776
      || | | | | | | | | | | | | | | | | | | | | |
Db     713 AAGCACGAAGGCTAACCATCTGCTACTCCTTGCAATTTTACGTATGTTTTTACCCTTCC 772

Qy     777 ATATCATGCGCAATTTGAGGATCGCCTCAGCCTG 811
      |||| | | | | | | | | | | | | | | | | | |
Db     773 ATATCTTGAGGGTCATTCGGATCGAATCTCGCCTG 807

```

Search completed: December 14, 2003, 13:22:08
Job time : 453 secs